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SEARCH REQUEST FORM

Scientific and Technical Information Center

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Include the elected species of utility of the invention. Defi	structures, keywords, synony	describe as specifically as possible the subjects, acronyms, and registry numbers, and cospecial meaning. Give examples or relevan laims, and abstract.	ombine with the concept or
Title of Invention:			
Inventors (please provide f	ull names):	<u> </u>	•
Earliest Priority Filing I	Date:		
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Jan Delaval
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Searcher Phone #: 4498	AA Sequence (#) 10	Dialog
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Date Searcher Picked Up: 412 07	Bibliographic	Dr.Link
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"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970).
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MEDLINE-82274238; PubMed-6287432;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
Nucleic Acids Res. 10.4071-4079(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Ponsting1 H., Hilschmann N.;
Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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MEDLINE-71064025; PubMed-5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., Edelman G.M.;
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MEDINE-710464027, PubMed-4923144;

Gall W.E., Edelman G.M.;

"The covalent structure of a human gamma G-immunoglobulin. X.
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BEDLINE-71064024; PubMed-5489771;
Cunningham B.A., Rutilabauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.;
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                                                                                                                                               "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9 - and 2.98 A resolution.";
Biochemistry 20:2361-2370(1981).
-!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.
-!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
-!- MISCELLANEOUS: RUE ALSO DIFFERS IN THE AMIDATION STATES OF 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
                                               Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal 1961 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02146; GHHU.
PDB; 1FC1; 15-JUL-92.
PDB; 1FC2; 15-JUL-92.
MIM; 147100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                          Deisenhofer J.;
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                                                                                                                                                                                                                                                               268-272
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE=81021548; PubMed=6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
"Primary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-77118561: PubMed-402363; Michaelsen T.E., Frangione B., Franklin E.C.; Michaelsen T.E., Frangione B., Franklin E.C.; "Primary structure of the 'hinge' region of human 1gG3. Probable quadruplication of a 15-amino acid residue basic unit."; J. Blol. Chem. 252:883-889(1977).
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21-UUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                           36106 MW; 3770EE106C2FA33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4e-51;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  97.1%; Score 568; 96.4%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS TO 12-97 OF PROTEIN WIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.1
Best Local Similarity 96.4
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                    281
284
296
301
                          330 AA;
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GC3_HUMAN
P01860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CH1 REGION.
-1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain; Immunoglobulin C region; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-i- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR ANOTHER GAMMA CHAIN SUBCLASS.
MISCELANBOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                                                                                                                                                                  SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
MEDLINE-82247835; PubMed-6808505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-1- SUBURIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIMER).
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REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC). MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.; "The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoglobulin G3."; Blochem. Biophys. Res. Commun. 71:907-914(1976).
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INTERCHAIN (WITH HEAVY CHAIN DII
INTERCHAIN 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HINGE.
CH2.
CH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J00231; AAA52805.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00410; IG_like; 1. SMART; SM00407; IGcl; 1.
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HSSP; P01857; 1FC1.
MIM; 147120; -.
                                                                                                                                                                                                                                                                                                                                                      gene deletion model
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CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVQVHNAKTK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-70207560; PubMed-4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=83157104; Pubmed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
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Pred. No. 7.1e-51;
POST-TRANSLATIONALLY
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                               /FTId=VAR_003896.
E69CBC95705B2F46 CRC64;
           OV -> EB (IN ZUC).
/FTId=VAR_003890.
P -> L (IN OMM).
/FTId=VAR_003891.
F -> Y (IN OMM).
T -> A (IN OMM).
/FTId=VAR_003892.
                                                                                                                                                                                                                                                FTIG=VAR_003895
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
REMOVED
                                                                                                                                                                                                                                  MISSING
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21-JUL-1986 (Rel. 01, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                     290 AA; 32331 MW;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
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95.5%;
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                                                          134
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HSSP; P01842; 7FAB.
MIM; 147130; -
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                          134
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P01861;
                                                                                                                                                                                                                                                                                                                     SEQUENCE
MOD_RES
                                                          VARIANT
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DISULFID
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MEDLINE-8423592; PubMed-6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
                                                                                                                                                                                                                111 APEFLGGPSVFLFPPKRKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170
                                                                                                                                                                                                     1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                              Ellison J.W., Hood L.E.;
"Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T., Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T., "Structure of human immunoglobulin gamma genes: implications for evolution of a gene family."; cell 29:671-679(1982).
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                                                                                       INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                       INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                        Score 541; DB 1; Length 327;
Pred. No. 2.4e-48;
3; Mismatches 6; Indels
                                                                                                                                          35940 MW; 3EDBD811EF208E7A CRC64;
 Pfam; PF00047; ig; 3.
SMART: SM00410; IG_like; 1.
SMART; SM00407; IGCl; 2.
SMOSTIE: PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
1G gamma-2 chain C region.
                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                      326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL). MEDLINE-81007873; PubMed=6774012; Wang A.-C., Tung E., Fudenberg H.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Fetal liver;
MEDLINE-83001943; Pubmed-6811139;
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                                                                                                                                                                   92.5%;
milarity 91.8%;
Conservative 3
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                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                      98
1110
2220
327
14
83
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; Biochem. J. 121:217-225(1971).
                                                                                        ECORONCE OF 1-85 AND 132-325 (MYELOWA PROTEIN ZIE).
MEDLINE-80001357; PubMed-113060;
Connell G.E., Parr D.M., Hofmann T.;
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Can. J. Blochem. 57:758-767(1979).
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                                                                                                                                                                                                                                                   SECUENCE OF 238-275 (ZIE).
MEDLINE=80114419; PubMed=118920;
Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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"The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications."; J. Immunol. 125:1048-1054(1980).
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DISULINE-69064124; PubMed-5782707;
Frangione B., Milstein C., Pink J.R.L.;
Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 25; 59; 60 AND 264-268 (ZIE). Hofmann T., Parr D.M.; Submitted (MAR-1980) to the PIR data bank.
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HINGE.
CH2.
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Eur. J. Biochem. 228:886-893(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-121 (DOT).
MEDLINE=95255298; PubMed=7737190;
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MEDLINE-72033500; PubMed-4940472;
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HSSP; P01857; lFC1.
MIM; 147110; -.
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Brueggemann M.;
Brueggemann M.;
Brolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74.473-482(1988).
PIR; PS0018; PS0018.
HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003609; Ig_like.
Ffam; PS000410; Ig_like.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGGl; 2.
PROSITE; PS00290; IG_MRC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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Sciurognathi; Muridae; Murinae; Rattus
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                AT OR NEAR THE COMPLEMENT-BINDING SITE.
REMOVED POST-TRANSLATIONALLY (PROBABLE)
S -> A (IN MYELOWA PROTEINS TIL & ZIE).
C-TYIG-AVR_003889.
C -> S (IN REF. 3).
C 310878C6878CF9C CRC64;
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                                                                                                                                                   Score 540; DB 1;
Pred. No. 3e-48;
3; Mismatches 3
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1999 (Rel. 38, Last annotation update)
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.6%; Score 460; DB 1; 75.2%; Pred. No. 5e-40; iive 16; Mismatches 1
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Mammalia; Eutheria; Rodentia;
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Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                              MEDLINE=71058471; PubMed=5538606; Birshtein B.K., Hussain Q.Z., Cebra J.J.; Birshtein B.K., Hussain Q.Z., Cebra J.J.; Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the balf-cystine joining heavy and light chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
antibodies.";
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MEDILINE-7036073. PubMed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig 1962
                                                                                                                                         Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                        (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
                   329 AA
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Submitted (APR-1975) to the PIR data bank
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MEDLINE=71058486; PubMed=5538616;
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MEDLINE=75036072; PubMed=4429665;
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MEDLINE=71058474; PubMed=4922544;
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                                                                                                                      Ig gamma-2 chain C region
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SEQUENCE OF 4-68.
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MEDIANDE-76135469; Pratt D.M., Mole L.E.;
Pratt D.M., Mole L.E.;
Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILTD-6403090; PubMed-6313520;
MEDINGLED K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit 1gG heavy chain from the recombinant
                                                                                                                      gamma
                                                                                   Gaps
                                                                                                        2 PELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP 61
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                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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Stockholm (1967).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 88-266 FROM N.A.
MEDLINE=83299917; PubMed=6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit IgG: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                   .;
                                                           Length 329;
                                                                                                                                                        REEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                      Score 458; DB 1; Length 32
Pred. No. 7.9e-40;
8; Mismatches 15; Indels
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
  178 178 N-LINKED (GLCNAC. ..).
248 308
329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;
                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                            323 AA
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MEDLINE=70110015; PubMed=5461106;
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Immunogenetics 18:387-397(1983).
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78.9%;
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P01870;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
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Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 REEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
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                                                                                                                                                                                                                                         D11 MARKER).
E15 MARKER).
REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 450; DB 1; 75.2%; Pred. No. 5.2e-39; iive 11; Mismatches 16.
                                                                                                                                                                                           Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 AA
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   entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                              35404 MW;
                                                                                                                                           Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                        HSSP, P01857; 1FC1.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_C1.
                                                       EMBL; M16426; AAA31289.1;
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82; Conservative
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                                                                           PIR; A02161; GHRB
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InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
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                               THESP, POLIST, 1872.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SWART; SW00410; IG_like; 1.
SWART; SW00400; IG_like; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                       Length 329;
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329 AA; 36228 MW; F45827174182BAD6 CRC64;
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01-AUC-1991 (Rel. 19, Last sequence update)
12-UUL-1999 (Rel. 38, Last annotation update)
15 gamma - 3 chain C region, membrane-bound form.
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Nucleic Acids Res. 11:6775-6785(1983).
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HINGE.
CH2.
-; NOT_ANNOTATED_CDS
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EBMBL; V01526; CAA24767.1; ALT_SEQ..
PIR; AQ2155; G3MSM.
HSSP; P01857; IFCI.
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Hes 79; Conserv
                    PIR; B02156; G3MSC
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DOMAIN
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MEDLINE-80012837; Pubmed-113776;
ROGERS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPRE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE=80202559; PubMed=6769752;
Mano Y. Yamawaki-Katacka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_raxID=10090;
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MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.;
"Clonjog and complete nucleotide sequence of mouse immunoglobulin game 1 chain gene.";
cell 18:559-568(1979).
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                    InterPro: IPR003600; Ig_like.
Prion, Pro0047; ig; 3.
SMART; SM00400; IG_like; 1.
SMART; SM00407; IGcl; 2.
PR051TE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Iransmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 437; DB 1; Length 398;
Pred. No. 1.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Indels
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
W; CF7F264B50A4B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.7%; Scor.
y 73.8%; pred. No. 1...
''ve 12; Mismatches
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region.
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HINGE.
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Best Local Similarity 73.8%
Matches 79; Conservative
InterPro; IPR003597; Ig_c1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 AA;
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P01868;
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                R EMBL; V00793; CAA24173.1; -
R EMBL; V00793; CAA24173.1; -
R EMBL; V00793; CAA24173.1; -
R EMBL; V00793; CAA24175.1; -
R EMBL; V00795; CAA24175.1; -
R EASP; P01842; 7FAB.
R GJYCOSUITEDB; P01868; -
R MGD; MGI:96446; Igh-4.
R InterPro; IPR003597; Ig_C1.
R Ffan; PF00047; Ig; 3
R SAART; SM00407; IGC1:2.
R PROSITE; PS00299; IGC,MHC; 1.
R PROSITE; PS00299; IG_MHC; 1.
R PROSITE; PS00299; IGC,MHC; 1.
                                                                                                                                     Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                Adetugbo K.; "Evolution of immunoglobulin subclasses. Primary structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 REEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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HINGE.
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                                                    murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978)
                                                                                                     DISULFIDE BONDS (MOPC 21).
MEDLINE=73008889; PubMed=5073237;
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P01869;
21-JUL-1985 (Rel. 01, Created)
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Best Local Similarity 70.69
watches 77; Conservative
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1198
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276
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324 AA;
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GCIM_MOUSE
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MEDLINE-8222190; PubMed-6283537;

MEDLINE-82222190; PubMed-6283537;

Yamawaki-Katacoka Y., Nakai S., Miyata T., Honjo T.;

Proc.

"Nucleotide sequences of gene segments encoding membrane domains of lamunoglobulin gamma chains.", 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U.S.A., 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U.S.A., 79:2623-2627(1982).

SPECIES FOR IG GANMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GANMA CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
                      MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                             MEDLINE-82197626; PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
"MRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 323-366 FROM N.A.
MEDLINE-82115295; Pubmed-6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
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HINGE.
CH2.
CH3.
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Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; V00793; CAA24172.1; -. EMBL; V00793; CAA24173.1; -. EMBL; V00793; CAA24174.1; -. PIR; B02159; GIMSM. HSSP; P01842; 7FAB.
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                                                                                                                                                                                                                                       SEQUENCE OF 323-393 FROM N.A.
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217
324
82
102
                                                                                                                                                gamma 1 chain gene.";
cell 18:559-568(1979).
SEQUENCE FROM N.A.
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218
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                                                                                                                                                                                               112 PEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQP 168
                                                                                                                                                     Gaps
                                                                                                                                                                         2 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dognin M.J., Lauwereys M., Strosberg A.D.;
Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of 191a and 191b allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- MISCELLANBOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-82037861; PubMed-6170065; Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.; Multiple differences between the nucleic acid sequences of the IGG2aa and IGG2ab alleles of the mouse."; Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                    3;
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                            Length 393;
                                                                                                                                                                                                                      62 REEOYNSTFRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                   Indels
                                                                               CYTOPLASMIC (POTENTIAL).
4CC88343B7A1CE27 CRC64;
                                              N-LINKED (GLCNAC. . .).
                                                                                                                            72.2%; Score 422.5; DB 1; 70.6%; Pred. No. 4.3e-36; iive 16; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, B allele.
                                                                                                                                                                                                                                                                                                      335 AA
                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                           43386 MW;
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Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                    Query Match
Best Local Similarity 70.6%
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104
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1198
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3357
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340
358
393 AA;
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DISULFID
                       DISULFID
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SEQUENCE
                                              CARBOHYD
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Ollo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                           119 APDILGGESVEIFPPRIKDVLMISLSPWVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] SEQUENCE FROM N.A. MEDLINES #10777755; Sikorav J.-L., Auffray C., Rougeon F.; Sikorav J.-L., Auffray C., Rougeon F.; Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA."; Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                          1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
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Bourgois A., Fougereau M., Rocca-Serra J.;
Botermination of the primary structure of a mouse IgG2a
immunoglobulin:amino-acid sequence of the Fc fragment. Implications
for the evolution of immunoglobulin structure and function.";
Eur. J. Blochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoscomis,
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Biochem. 30:452-462(1972).
                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                  Score 418; DB 1; Length 335;
Pred. No. 1e-35;
                                                                                                                                                                                18; Indels
                      FA3382792CBB13C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-WAY-2000 (Rel. 39, Last annotation update) Ig gamma-2A chain C region, A allele.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 01, Created)
(Rel. 01, Last sequence update)
                                                                                                                                                                            17; Mismatches
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MEDLINE=73056887; PubMed=4565406;
1
36596 MW;
                                                                                                                  71.5%;
68.2%;
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                                                                                 Query Match
Best Local Similarity bo...
And 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYELOMA PROTEIN MOPC 173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                      335 AA;
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30-MAY-2000
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-88166903; Pubmed-3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Brueggemann M. Delmastro-Galfre P., Waldmann H., Calabi F.;
Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNR: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
4C38138BFAED3FF0 CRC64;
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.9%; Score 415; DB 1; Le
69.1%; Pred. No. 2.6e-35;
...sematches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2C chain C region.
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                                                        EMBL; J00471; AAB59661.1; ALT_INIT
                                                                         PIR; A02154; G2MSAM.
HSSP, P01857; 1FC1.
MGD; MGI:96443; 1Gh-1.
InterPro; IPR003506; 1g_MHC.
InterPro; IPR003597; 1g_C1.
InterPro; IPR003600; 1g_like.
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                                                                                                                                                                               Pfam; PF00047; 19; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
                                                                                                                                                                                                                                      PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44020
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Best Local Similarity 69.1%
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
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82
107
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399 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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P20762;
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GCC_RAT
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          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Yamawaki-Katadoka Y., Nakai S., Miyata T., Honjo T.;

Proc. Natl. Acad. Sci. U. S.A., 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U. S.A., 79:2623-2627(1982).

-1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MENA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                               CHAIN).
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 415; DB 1; Length 330; Pred. No. 2.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                   REMOVED POST-TRANSLATIONALLY B84361C5445A6864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAM_MOUSE STANDARD; PRT; 399 AA. p01865; 21-JUL-1986 (Rel. 01, Created) 01-AUG-1991 (Rel. 19, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Ig gamma-2A chain C region, membrane-bound form. Mus musculus (Mouse).
                                                                                                                                                                    PROBLES SWOOT 15. 19. 3. SWART: SWOOT 15. 11ke; 1. SWART: SWOOT 16. 11ke; 1. SWART: SWOOT 16. 16. 1. 1. SPROSTE; PSOO290: IG_MHC; 1. Immunoglobulin domain; Immunoglobulin C region.
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                                                                                                HSSP, P01842; 7FAB.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_C1.
Interpro; IPR003600; Ig_like.
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69.1%;
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330 AA;
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INTERCHAIN (WITH A LIGHT CHAIN).
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70.1%; Score 410; DB 1; Length 329;
Best Local Similarity 69.8%; Pred. No. 6.8e-35;
Matches 74; Conservative 15; Mismatches 17; Indels
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HSSP; p01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
Immunoglobulin domain; Immunoglobulin C region.
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Search completed: June 21, 2002, 09:00:25 Job time: 1449 sec

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Q96dk0 homo sapien Q9brv0 homo sapien

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Scoring table:

Searched:

Database

Perfect score:

Run on:

Sequence:

096169 homo sapien 096661 homo sapien 0948w4 mus musculu 091v32 m adult mal

29v787 drosophila

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[1]
SEQUENCE FROM N.A.
MEDLINE=21477448; PubMed=11593034;
Hu Z., Garen A.;
Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
EMBL; AF272774; AAK58666.1; -.
EMBL; AF272774; AAK58666.1; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 568; DB 4; Length 701;
Pred. No. 1.8e-55;
2; Mismatches 2; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
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96.48;
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Oggic4 mus musculu
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Q95m34 equus cabal
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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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Query Match

Result 8 474 422.5 422.5

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Length 437;
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70.6%; Pred. No. 2.6e-39;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (SCFV).";
Submitted (MAY-11999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIS2372; AAA40243.1;
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98383416; PubMed-9717671; Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.; I. Leibold W., Radbruch A.; Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-119(1998).
EBMBL; A3300675; CAC44624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 APELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFNWYMDGVEVRTATTR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APELLGGPSVFLFPPKPKDTLMISRTPEVICVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.0%; Score 474; DB 6; Length 337; 76.4%; Pred. No. 3e-45; 1ive 17; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
10-DEC-2001 (TrEMBLrel. 19, Last annotation update)
10-DEC-2001 (AMDIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam, PF00047; Ig; 4.
SMART; SM00406; IGY; 1.
SMART; SM00410; IG_like; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                              Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 84;
                                                                                                                                                  (FRAGMENT).
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sequence
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SEQUENCE
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Q9R1A4;
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                                                                                                                                                                                                                                                                                                                                                                                                                Wagner
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Q9R1A4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                       2 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP 61
      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.2%; Score 422.5; DB 11; Length 463; 70.6%; Pred. No. 2.8e-39; ive 16; Mismatches 13; Indels 3;
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L Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

E EMBL; BC003435; AAH03435.1; -.

R EMESP; P01842; 7FAB.

R InterPro; IPR003599; Ig.,

R InterPro; IPR003500; Ig_like.)

R InterPro; IPR003500; Ig_like.)

R InterPro; IPR003506; Ig_MHC.

DR SMART; SM00407; IG; 2.

DR SMART; SM00407; IG; 2.

DR SMART; SM00407; IG; 2.

DR SMART; SM00407; IG_like; 1.

DR SMART; SM00407; IG_like; 1.

DR SMART; SM00406; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 REEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 REEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                       282 REEQPNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 330
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Disclosure; Page 33-34; 41pp; English.

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This protein comprises an immunoglobulin (Ig) C-gamma-3 region.
The invention provides a method for the production of tumour-
specific Ig derived from a B-cell lymphoma patient. In the novel
method expression plasmids containing the patient's VH region(s)
joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)
cequence and expression plasmids containing the patient's VL
region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2
cegion(s) joined to either a C-kappa (see AAT97190) or C-lambda-2
cegion(s) joined to either a C-kappa (see AAT97190) or C-lambda-2
cepion(s) joined to either a C-kappa (see AAT97190) or C-lambda-2
cepion(s) joined to since are cotransfected along with a selectable and
transfected cells are then subjected to selection and amplification.
The method permits the production of a multivalent vaccine which
reflects the degree of somatic variation found within the patient's
tumour. These novel multivalent vaccines provide superior vaccines
                                                                                                                                                                                                                                                                                                                                                                                                         1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atibody-based fusion proteins, used for the delivery of e.g. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IgG3; C-gamma-3; antibody; fusion protein; circulating half-life;
                                                                                                                                                                                                                                                                                                                                        Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "the identity of these residues is not specified"
immunoglobulin molecules derived from B cell lymphoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                     Score 585; DB 18;
Pred. No. 6.1e-50;
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                               Example 10; Page 123-124; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lo K, Wesolowski J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 1..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY31671 standard; Protein; 494 AA.
                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                            Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lan Y,
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-527594/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IgG3 chain C.
                                                                                                                                                                                                                                                                                    377 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gillies SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-SEP-1999
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY31671;
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Gaps

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The present sequence represents the constant region of human IgG isotype 3 (IgG3, C-gamma-3). C-gamma-3 and C-gamma-1 (see AAY1669) bind Fer receptors with high affainity, whereas C-gamma-4 (see AAX31672) has 10-fold lower binding affainity and C-gamma-2 (see AAX31672) has 10-fold lower binding affainity and C-gamma-2 (see AAX31670) does not bind to Fe receptor gamma-1. The invention of antibody-based fusion proteins with enhanced circulating half-lives. The fusion proteins lack the ability to bind to immunoglobulin Fc receptors, either as a consequence of the antibody isotype used for protein construction, i.e. a C-gamma-2 constant region (Fc) or a C-gamma-4 Fe receptor, or through directed mutagenesis of antibody isotypes that normally bind Fe receptors, i.e. C-gamma-1 or C-gamma-1 introduction of a mutation or a deletion at one or c-gamma-3. Introduction of a mutation or a deletion at one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APELLGGPSVFLFPPRPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                       Or C-gamma-3. Introduction of a mutation or a deletion at one or note amino acid of C-gamma-3 selected from Leu281, Leu282, G1y284, Ann344, and Pro378, produces an ig heavy chain having reduced binding affinity for an Fc receptor. The methods protein such as a cytokine, e.g. tumour necrosis factor (TNF), an interleukin or a lymphokine such as a lymphotoxin or a colony stimulating factor, a ligand-binding protein, e.g. CD4, CTLA-4, TNF receptor or an interleukin receptor, or a protein toxin (claimed). The fusion proteins are used to deliver selectively the second non-1g protein to a target cell in vivo so that the second non-1g protein can exert a localised biological effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgG antibody; light chain; Fc region; effector function; cancer; allergy; asthma; LFA-1-mediated disorder; tumour; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Fc region-containing polypeptides that have altered effector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of native IgG Fc region humIgG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 585; DB 20; 100.0%; Pred. No. 8.4e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 100.0%; Pred. No. 8.4
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB07477 standard; protein; 218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-2000; 2000WO-US00973.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-476035/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 110; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200042072-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

June 21, 2002, 08:36:07; Search time 224.82 Seconds (without alignments) 54.346 Million cell updates/sec Run on:

US-09-674-857-6 585 1 APELLGGPSVFLFPPRFKDT......CKVSNKALPAPIEKTISKTK 110 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

747574

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /SIDSJ/gcgdata/hold-geneseq/genesegp-embl/AA1980.DAT:*
2: /SIDSJ/gcgdata/hold-geneseq/genesegp-embl/AA1981.DAT:*
3: /SIDSJ/gcgdata/hold-geneseq/genesegp-embl/AA1981.DAT:*
3: /SIDSJ/gcgdata/hold-geneseq/genesegp-embl/AA1981.DAT:*
4: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
5: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
6: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
7: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
8: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
9: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
110: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
112: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
113: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
114: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
115: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
116: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
117: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
118: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
119: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
119: /SIDSJ/gcgdata/hold-geneseqy-embl/AA1990.DAT:*
119: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
119: /SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
119: /SIDSJ/gcgdata/hold-geneseqy-embl/AA1990.DAT:*
119: /SIDSJ/gcgdata/hold-geneseqy-geneseqp-embl/AA1990.DAT:*
119: /SIDSJ/gcgdata/hold-geneseqy-geneseqp-embl/AA1990.DAT:* A_Geneseq_032802:* 111: 123: 133: 144: 176: 196: 220: 221: 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Immunoglobulin C-g	Human IgG3 chain C	Amino acid sequenc	Human IgG3. Homo	Human IgG3 Fc regi	Undefined ORF3 enc	Human immunoglobul	Undefined ORF2 enc	Human IgGl Fcgamma	Immunoglobulin G1	Human immunoglobul
	QI	AAW37345	AAY31671	AAB07477	AAB67204	AAB76424	AAR41713	AAR27680	AAR41684	AAY42621	AAR87023	AAR97264
	93	18	20	21	22	22	14	13	14	20	16	17
	Query Match Length DB	377	494	218	218	218	110	110	110	116	212	212
P	Query	100.0	100.0	99.3	99.3	99.3	97.4	97.1	97.1	97.1	97.1	97.1
	Score	585	585	581	581	581	570	568	568	568	568	568
	Result No.	, ,	7	m	4	'n	9	7	œ	6	10	11

212 17 AAW02305 212 20 AAW7354 212 20 AAW7354 213 20 AAW7357 213 21 AAY9937 213 21 AAY9937 213 21 AAY9937 213 21 AAY9937 213 21 AAB03809 213 22 AAR72750 218 22 AAR67201 218 22 AAR67201 218 22 AAR67201 218 22 AAR67201 224 8 AAF70173 224 8 AAF70173 224 8 AAF86780 224 8 AAF86780 224 8 AAF86780 224 8 AAF86780 225 21 AAR86890 228 21 AAR86890 232 21 AAR86897 232 22 AAR80897 233 22 AAR80897 234 21 AAR80897 235 22 AAR80897 237 22 AAR80897 238 23 AAR80897 238 238 248 248 248 248 248 248 248 248 248 24	Human IgG1 Fc regi	Human immunoglobul	IgG1 Fc protein us	n IgGl Fc	Human IgG1 Fc regi	Human immunoglobul	Human immunoglobul	Fc region of human	Fc region of human	Human immunoglobul	Native IgG Fc regi	Native IgG Fc regi	0	Human IgG Fc 1 all	Human IgG1 non-A F	Human IgG1 A allot	Sequence of human	lobulin	Human IgG1 Fc prot	IgG1 Fc	Human IgG1 Fc regi		Human IgGgammal hi	Human immunoglobul					Human immunoglobin	FC (I		Ĥ.	inhibito	Fc-TMP protein seq
	AAW02305	AAW47354) AAY23637	AAW92411	. AAY99937	AAY97182	AAY97250	. AAB03809										۹													_		1 AAB17957	1 AAB16958
	12 17	212 19	212 20	12 20	12 21	12 21	12 21	12 21	7	7	7	7	7	7	7	~							7	7	7	7	7	~	~	7	~	7	243 2.	247 2
	97.1	97.1	97.1	97.1	97.1	97.1	97	97.	97.1	97	97	97	97	97	97	97	97	97.1	97	97	97	97	97.	97.	97.1	97.	97.	97.	97.	97.	97.	97.	97.	97.
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5568 977 5568 977	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	. 27		29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour; gene amplification; immunotherapy; therapy; immunoglobulin; C-gamma-3; constant region. AAW37345 standard; Protein; 377 AA. Immunoglobulin C-gamma-3 region. 97WO-US07039. 96US-0761277. 96US-0644664. (first entry) WO9741244-A1. Homo sapiens 06-DEC-1996; 01-MAY-1996; 11-MAY-1998 25-APR-1997; 06-NOV-1997. AAW37345; RESULT AAW37345 

Multivalent vaccine to treat B cell lymphoma or leukaemia comprises at least 2 different recombinant variable regions of N-PSDB; AAT97188

(GENI-) GENITOPE CORP.

WPI; 1997-549743/50.

Denney DW;

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RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL, BC017356; AAH17356.1; -
KW Hypothetical protein.

SQ SEQUENCE 618 AA; 67758 WW; 96DBD4C7C696E0A6 CRC64;

Query Match

Query Match

Best Local Similarity 29.7%; Pred. No. 9.9e-08;

Matches 30; Conservative 24; Mismatches 45; Indels 2; Gaps 2;
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Dp Qy

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10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNST 69

Search completed: June 21, 2002, 08:59:32 Job time: 1631 sec

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TISSUE=LYMPH, AND LYMPHOMA; Strausberg R.;
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Matches 30; Conservative
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NCBI_TaxID=9606;
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11D 6646

099 DPT 011D 099 DPT 099 DPT 099 DPT 099 DPT 099 SP 099 SP
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:20337).
UMRNOWN (PROTEIN FOR MGC:20337).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 597;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.6%; Score 144; DB 4; Length 59
29.7%; Pred. No. 9.5e-08;
Live 24; Mismatches 45; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ll protein.
597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                         InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
SNART; SM00407; IG21; 4.
SNART; SM00406; IGv; 1.
SNART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SPOUENCE 597 Aa; 65274 MW; 2DAFABFB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          096BB9 PRELIMINARY; PRT; 597 AA. 096BB9; 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) HYPOTHETICAL 65-0 KDA PROTEIN.
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TISSUE=PRIMARY B-CELLS FROM TONSILS;
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                           19_c1.
19_like.
19_MHC.
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Best Local Similarity 29.7%
Matches 30; Conservative
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           finterPro; IPR003597;
                                                          InterPro; IPR003600;
InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                       363 VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRONGEAVKTHTNISESHPNAT 420
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                    Length 613;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009851; AAH09851.1; -.
SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
SECUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96AA6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 67.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01NKNOWN (PROTEIN FOR MGC:15420).
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29.7%; Pred. No. 9.8e-08;
tive 24; Mismatches 45
                                                                                                                                                                                                                 Query Match 24.6%; Score 144; DB 4; Best Local Similarity 29.7%; Pred. No. 9.8e-08; Matches 30; Conservative 24; Mismatches 45
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SEQUENCE FROM N.A.
TISSUE=PRIMARY B-CELLS FROM TONSILS;
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PRT;
                                     PRT;
                                     PRELIMINARY;
                                                                                                                                                                                           TISSUE=RHABDOMYOSARCOMA;
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                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        TISSUE-LYMPHOMA;
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                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                                                                                       Strausberg R.;
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                                     Q9BQB8
             10
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            RESULT
Q9BQB8
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                                                                                                                                                                                                                                                                                 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNST 69
                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                Length 473;
                                                                                                                                                                                                                                                                                                                                  61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                               Query Match 24.6%; Score 144; DB 4; Length 375; Best Local Similarity 29.7%; Pred. No. 5.3e-08; Matches 30; Conservative 24; Mismatches 45; Indels
                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                       Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001); -. Hypothetical protein. SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO04475; AAH04476.1; -.
HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41314 MW; B1A0A0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA.PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 FRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 FSAVGEASICEDDWNSGERFTCTVTHTDLDSPLKQTISRPK 244
                                                                                                                                                                                                                            Query Match
69.7%; Score 408; DB 11;
Best Local Similarity 67.3%; Pred. No. 1.2e-37;
Matches 74; Conservative 15; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                          375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; ig; 3.
SMART; SM00407; IGcl; 3.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL 41.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-LYMPH, LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein SEQUENCE 375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BSZ1;
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368 VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNAT 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC006180: AAH06180.1; -.
EMBL: BC001872; AAH01872.1; -.
                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK 466
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24.6%; Score 144; DB 4;
Best Local Similarity 29.7%; Pred. No. 9.5e-08;
Matches 30; Conservative 24; Mismatches 45.
597 AA.
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InterPro; IPR003600;
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ID 09
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                                      A Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Rabischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Rabischmann W., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Rabis Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,
Rabis J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Rabis J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Rabis J., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Ryordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Ryasaki R., Ryasaki S.,
Ryasaki R., Saboris A., Yoshida K., Rawaji H., Kohtsuki S.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                    Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.5%; Score 418; DB 11; Length 473; 68.2%; Pred. No. 9.2e-39; tive 17; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:9644; Ighi.

MGD; MGI:9643; Ighi.

InterPro; IPR00359; Ig.

InterPro; IPR003600; Ig_like.

InterPro; IPR00360; Ig_MRC.

InterPro; IPR00356; Ig_W.

RARRT; SM0040; IG; 4.

SMART; SM0040; IGC; 3.

SMART; SM00406; IGC; 1.

SMART; SM00406; IG_W: 1.

SMART; SM00406; IG_W: 1.

SMART; SM00406; IG_W: 1.

SMART; SM00410; IG_like; 1.

REQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                STRAIN-C57BL/6J; TISSUE-PANCREAS;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1;
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
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Best Local Similarity 68.28
Matches 75; Conservative
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SEQUENČE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Q99L31;
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Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 THREDINSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPK 366
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InterPro; IPR003597; 19_cl.
InterPro; IPR003606; Ig_like.
InterPro; IPR003066; Ig_like.
InterPro; IPR003596; Ig_like.
InterPro; IPR00407; Ig_like.
InterPro; IPR00407; Ig_like.
InterPro; IPR00407; Ig_like.
InterPro; IPR00407; Ig_like.
InterPro; IPR04107; Ig_like.
InterPro; IPR051116; Ig_like.
InterPro; IPR05116; Ig_like.
INTERPRO; IRR05116; IRR05116; IRR05116; IRR05116; IRR05116; IRR051
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -.
HSSP; P01842; 7FAB.
InterPro; IPR003599; Ig.
                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 18100660009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 70.3%; Score 411; DB 11; Best Local Similarity 69.1%; Pred. No. 5.6e-38; Matches 76; Conservative 14; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.3%; Score 411; DB 11;
69.1%; Pred. No. 5.7e-38;
Live 14; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Best Local Similarity 69.1%
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus (Mouse).
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AAB07474-78 represent native IgG Fc regions. The proteins are used to produce Fc region-containing polypeptides that have altered effector function as a consequence of one or more amino acid modifications in the Fc region. The variant polypeptides are useful for treating cancer, allergic conditions such as asthma (with an anti-1gE antibody), and LEA-1-mediated disorders. Where the polypeptide binds the HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a hengn or malignant tumour characterized by overexpression of the HER2 receptor. Such cancers include breast cancer, aguamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, badder cancer, hepatoma, colon cancer, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, hypoid cancer, hepatic carcinoma and various types of head and neck cancer.
on due to one or more amino acid modifications in the Fc region, in the treatment of cancer and allergic conditions such as % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\}
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Pred. No. 8e-50;
1; Mismatches 0; Indels
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Matches 109; Conservative
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      function
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Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain

Lazarus RA;

Dennis MS,

WPI; 2001-123106/13.

The present invention relates to a fusion protein, comprising

Disclosure; Fig 2; 69pp; English

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This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides represented in AAB76510 and AAB76432. AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences used in the lsolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, diseases of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, isoraemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafiness; Meniere's disease; diabetic neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                             2 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfkwyvdgvevhnaktk 61
                                                                                                                                                                                                                                                                             1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (Ib). The hybrid molecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used. For example the peptide ligand can bind ErbB2. The peptide ligand may bind to and inhibit the activity associated with a particular target molecule.
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                                                                                                                                                                                                     22; Length 218;
                                                                                                                                                                                                                                                                                                                                                                      61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                 Score 581; DB 22
Pred. No. 8e-50;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IgG3 Fc region amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB76424 standard; Protein; 218
                                                                                                                                                                                                     99.3%;
99.1%;
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Best Local Similarity 99.1
Matches 109; Conservative
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                                                                                                                                                 218 AA;
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                                                                                                                                                 Sequence
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61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
  AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. also be used for diagnostic methods.
                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pAH4807. This vector represents the cloning of the human gamma isotype, gamma-3 with the variable region of the murine monoclonal antibody 128.1. This plasmid enrocles a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody which hinds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to prevent neurological disorders eg. brain tumours.
Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAR41710-14 are encoded by the expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                    Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy: light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                                                             Gaps
                                                                                                                                                      1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                    2 apellggpsvflfppkpkdtlmisrtpevtcvvdvshedpevqfkwyvdgvevhnaktk 61
                                                                                                                           ;
0
                                                                                              Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody conjugates specific for transferrin receptor – used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                           PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                        0; Indels
                                                                                               Score 581; DB 22;
                                                                                                              Pred. No. 8e-50;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Undefined ORF3 encoded by plasmid pAH4807.
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                                                                                                                                                                                                                                                                                                         AAR41713 standard; Protein; 110 AA.
                                                                                              99.3%;
99.1%;
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                                                                                                                           Conservative
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N-PSDB; AAQ43847.
                                                                                                              Similarity
                                                      218 AA;
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                                                                                                                           109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders
                                                                                                                                                                                                                                                                                                                                   AAR41713;
                                                       Sequence
                                                                                               Query Match
                                                                                                              Best Local
Matches 1(
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                                                                                                                                                                                                            61
                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                            AAR41713
                                                                                                                                                                                                                                                                                RESULT
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or 17. The inventor's propose eliminating these allotypes by amino acid changes to agree with the sequences of 1gG2, 1gG3 and 1gG4. None of the allotype sites (1, 2 and 17) are located within the CH2 domain. New 'isoallotypes' should be suitable for therapeutic use in all patients. See AAR27678-R27681.
                                                     Gaps
                                                                                              1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                        1 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevgfkwyvdgvevhnaktk 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktk 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In humans, IgG1 may exist as either of two allotypes at site 1, 2
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       Length 110;
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                                                                                                                                                                                       61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                               Humanised antibodies having modified allotypic determinant useful for matching allotypes in therapy with decreased likelihood of causing undesirable immune responses
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isoallotype; IgG1 Glm(1,2,17); anti-allotype response; humanised Ab.
       DB 14;
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Score 570; DB 14
Pred. No. 4.4e-49
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Pred. No. 7e-49;
                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunoglobulin IgG1 CH2 region.
                                                                                                                                                                                                                                                                                                                                                 AAR27680 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4c; 57pp; English
    97.4%;
98.2%;
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96.48;
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                                                  Conservative
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Best Local Similarity
Matches 106; Conserv
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 AA;
  Query Match
Best Local Simi.
Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clark MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pAH4602. This vector contains open reading frames encoding the heavy chain variable region (VH) of the antibody 128.1, an ampicillin resistance gene and a histidine (histidinol) selection marker.

Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin conhancer and the human gammal. Constant region (CH). The VH region of 128.1 was achieved by digesting the plasmid and the product with EcoRV and Nhel. The VH gene was inserted in frame with the human comman and CH region CH at the 3' end of the VH-J region by means of a Nhel site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This can thibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AlbS, stroke, equilessy, parkinsons and Alzheimers disease. It may also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAR41682-85 are encoded by the expression vector,
                                                                                                                                                                                                                                                            Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody conjugates specific for transferrin receptor – used for diagnosis and treatment of cancer, AIDS and neurological disorders
Disclosure; Fig 11K; 151pp; English.
                                                                                                               Ą
                                                                                                                                                                                                                        Undefined ORF2 encoded by pAH4602.
                                                                                                             AAR41684 standard; Protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0800458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US10206
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALKE-) ALKERMES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-196742/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ43844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-1991;
                                                                                                                                                                                       20-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                WO9310819-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Friden PM;
                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                  AAR41684;
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                 61
                                                                                             AAR41684
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The invention provides immunoglobulin E (IgE) antagonists comprising one or more of the FcepsilonRI receptor-binding determinant sites of human ligE. The antagonists include IgE variants comprising an immunoglobulin template and binding determinant sequences (bds) CDbds, EFbds and the sequence shown in AAY42581. The CDbds (CD loop binding determinant sequence) are selected from the sequences shown in AAY42580. The sequences shown in AAY42567 v42577 and the EFbds (EF loop binding determinant sequence) are selected from sequences shown in AAY42578 v42580. The variants are useful in raising and screening anti-IgE antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment and prophylaxis of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IgE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; bds;
                                                                                                                                                                                                                                                                                                                                                                          IgE; antagonist; FcepsilonRI receptor; human; bds
binding determinant sequence; anti-1gE antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 568; DB 20;
Pred. No. 7.5e-49;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Column 61-62; 37pp; English.
                                                                                                                                                                              Š
                                                                                                                                                                       AAY42621 standard; protein; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0232539
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94US-0178583
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                                                                                                                                                                                                                                                                                                                            Human IqG1 Fcgamma2 region.
                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 96.4
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jardieu PM, Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-579941/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AA;
                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                      receptor-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                           allergic disease
                                                                                                                                                                                                                                                                           10-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1999.
                                                                                                                                                                                                                          AAY42621;
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                                                                                                                                                  AAY42621
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Score 568; DB 14 Pred. No. 7e-49; 2; Mismatches

97.18; 96.48;

Query Match 97.1 Best Local Similarity 96.4 Matches 106; Conservative

DB 14; Length 110;

1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60 

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a superantigen.
                                                                                                                                                                                                                                                                                                                                                                                fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                    14-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-1996
                                                                                                                                                                                        AAR97264;
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61
                                       74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used in creating a BLLE2-immunoglobulin FC fusion protein (BLE2/FC).

BLEP2 is a Epstein-Barr virus (BBV) protein. To create BLLE2/FC, this sequence, the leader sequence of mouse interleukin-7 (1L-7) (see

AARB7021), a Flag octapeptide (see AARB7022) and a flexible linker (see

AARB7024) are joined to the extracellular domain (residues 34 to 223) of

the BLLE2 sequence (see AARB7020). The BLLE2/FC fusion protein

containing this sequence is referred to in claim 4. BLE2 proteins

containing this sequence is referred to in claim 4. BLE2 proteins are

members of the C-type lectin family. The C-type lectin domain is found

in type II membrane proteins. The BLLE2 protein is capable of binding

the beta chain of a major histocompatibility complex (MHC) class II

antigen. Fusion proteins with an oligomerising zipper domain (OZD).

Instead of an immunoglobulin Fc region, can also be created. BLLE2

proteins inhibit antigen-specific antibody formation, proliferation of

blood mononuclear cells and cytotoxic T cell responses. They also

certified sclerosis and systemic lupus erythematosus. Also, for treating

allergy or asthma. They can be used for treating or preventing

allergy or asthma. They can be used for treating or preventing

allergy or asthma. They can be used for treating or preventing

allergy or sthma. They can be used for treating or preventing

clisease, especially EBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                      antigen;
                                                                                                                                                     BZLF2; epstein-barr virus; EBV; C-type lectin; beta chain; MHC; antigen; major histocompatibility complex; immunoglobulin; cytotoxic T cell; autoimmune disease; myasthenia gravis; multiple sclerosis; allergy; systemic lupus erythematosus; organ transplant rejection; asthma; IL-7; tissue transplant rejection; therapy; cancer; viral disease; mouse; inteleukin-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the human immunoglobulin G1 Fc region, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epstein-Barr virus BZLF2 fusion proteins - used for treating e.g. auto-immune disease, transplant rejection, allergy, asthma, cancer or viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Farrah TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comeau MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.1%; Score 568; DB 16; 96.4%; Pred. No. 1.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Armitage RJ, Cohen JI,
r LM, Spriggs MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 38-39; 51pp; English.
    AAR87023 standard; protein; 212 AA.
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(USSH ) US NAT INST OF HEALTH.
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                                                                                                                             Immunoglobulin G1 Fc region
                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-393086/50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hutt-fletcher LM,
                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            W09530015-A2
                                                                                   11-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                28-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                         AAR87023;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated Herpes virus Saimiri 14 proteins - useful for treating autoimmune disorders, transplant rejection, allergy, asthma, cancer or viral disease
                                                                                                                                                                                                                                                                                                                                                                        HVS14; major histocompatibility complex; MHC; Class II; allergy; binding protein; inhibition; antigen presentation; superantigen; treatment; cancer; viral disease; immunoglobulin; IgG1; Fc region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a human immunoglobulin G1 Fc region, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can form a claimed fusion protein with the Herpesvirus saimiri (HVS) major histocompatibility complex (MMC) class II binding protein, HVS14. The fusion protein can be used to treat cancer or viral disease, as HVS14 inhibits antigen presentation, or acts as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1.5e-48;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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                                                                                                                                                                           AA.
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                                                                                                                                                                                                                                                                                                                       Human immunoglobulin G1 Fc region.
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                                                                                                                                                                        AAR97264 standard; protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.1%;
Best Local Similarity 96.4%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US15948.
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                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-287183/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW02305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXX
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence was used in the preparation of a synthetic construct containing the Epstein-barr virus (BBV) BLLF2 protein, which is capable of binding a beta-chain of a major histocompatibility complex (MHC) class II antigen. The protein can be used to inhibit antigen-specific antibody formation, peripheral blood monouclear cell proliferation and cytotoxic T-cell responses, e.g. in the prevention or treatment of autoimmune diseases, transplant rejection, allergies or asthma,
                                                                                                                                                                                                                                                                                                                                                                                         complex class II beta chain, useful for treating, e.g. auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BZLF2 protein; beta chain; blood mononuclear mononuclear cell; Class II major histocompatibility complex antigen; proliferation; cytotoxic T cell response; antigen specific response; asthma; autoimmune disease; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                             Epstein-Barr virus protein - binds to major histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 568; DB 19; Length 212;
Pred. No. 1.5e-48;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IgG1 Fc protein used to make BZLF2 fusion proteins.
                                                                                                                                                                                                 Cohen JI, Comeau MR, MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Columns 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY23637 standard; protein; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        diseases or transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0430633.
94US-0235397.
97US-0936854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.18;
96.48;
95US-0430633
                                                        95US-0430633
94US-0235397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0936854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 96.4<sup>1</sup>
Matches 106; Conservative
                                                                                                                                                                                                          Armitage RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and as a super-antigen
                                                                                                                                               (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                  WPI; 1998-192827/17.
                                                                                                                                                                                                                                      Hutt-Fletcher LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1994;
24-SEP-1997;
28-APR-1995;
                                                           28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5925734-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-1999
                                                                                                                                                                                                    Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The human IgG1 Fc region (AAW02305) can be used as a fusion partner for interleukin-17 receptor (IL-17R) proteins (see also AAW04184-85), allowing purification of recombinant IL-17R using protein A or protein G affinity chromatography. Fusions between Fc and HVS13 (see also AAW02387), a viral homologue of IL-17, and between Fc and murine CTLA8 (AAW02386) were used to identify calls that express the murine IL-17R. Selected murine thymoma EL4 cells were used as a source of murine IL-17R cDNA (AAT33800).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVOFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding interleukin-17 receptor - useful for regulating immune and inflammatory responses, or to suppress graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EBV; BZLF2; beta-chain; major histocompatibility complex; MHC; class II; antigen; prevention; treatment; autoimmune disease; transplant rejection; allergy; asthma; super-antigen; IgG1; Epstein-barr virus; human; immunoglobulin G1; Fc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.1%; Score 568; DB 17; Length 212; 96.4%; Pred. No. 1.5e-48; 1ve 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IgG1; interleukin-17 receptor; IL-17R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunoglobulin G1 Fc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW47354 standard; protein; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 33; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                          96WO-US04018
                                                                                                                                                                                                                                                                                                                                                                                      95US-0538765
                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0410535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.4
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spriggs MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP.
                        Human IgG1 Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-443184/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 AA;
                                                                                                                                                                                                       WO9629408-A1.
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                          21-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fanslow WC,
                                                                                                                                                                                                                                                                  26-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW47354;
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RESULT 13 AAW47354

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Gaps

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                                                                                                                               The present sequence represents a protein used to create fusion proteins with the Epstein-Barr virus BZLF2 proteins of the invention. The BZLF2 protein is capable of binding to a beta chain of a class II major histocompatibility complex antigen to inhibit an antigen-specific response. BZLF2 is useful for inhibiting antigen-specific antibody and cytotoxic T cell responses. BZLF2 is also useful for inhibiting undesirable antigen specific responses, e.g. in the treatment or prevention of asthma; for preventing or treating autoimmune disease; and for preventing tissue or organ transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T cell proliferation; T cell activation; organ; graft; rejection; autoimmune disease; allergy; asthma; treatment; inflammatory disease; B cell proliferation; immunogen; IgG1; Fo.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iso'ated interleukin-17 receptor DNA - used to develop products for treating e.g. organ or graft rejection, autoimmune disease, allergy, asthma or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                          Score 568; DB 20; Length 212;
Pred. No. 1.5e-48;
2; Mismatches 2; Indels
   Comeau MR, Farrah TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alderson M, Armitage RJ, Cohen JI,
Hutt-Fletcher LM, Spriggs MK;
                                                                                                   Claim 2; Column 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW92411 standard; Protein; 212 AA.
                                                                       Epstein-Barr virus BZLF2 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IgG1 Fc protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yao
                                                                                                                                                                                                                                                                                                                                         Query Match 97.1%;
Best Local Similarity 96.4%;
Matches 106; Conservative
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95US-0410535,
95US-0538765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fanslow WC, Spriggs MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP.
                                            WPI; 1999-418295/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-152766/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5869286-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-1999
                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW92411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
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                                 This sequence represents a human IgG1 Fc fragment which is used in the construction of a fusion protein with human interleukin-17 receptor (IL-17R). IL-17R polypeptides have immunoregulatory activity. They can be used for inhibiting T cell proliferation, or for inhibiting T cell activation. In particular they can be used for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. They can also be used for the prevention or treatment of inflammatory disease in proliferation or immunoglobulin screttion. The IL-17 polypeptides can also be used as immunogens, reagents in in vitro assays, or as binding agents for affinity purification procedures.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                          Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                        97.1%; Score 568; DB 20;
96.4%; Pred. No. 1.5e-48;
iive 2; Mismatches 2;
Example 1; Column 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 96.4
Matches 106; Conservative
                                                                                                                                                                                                                                                                                  212 AA;
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                            Query Match
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us-09-674-857-7.rpr

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June 21, 2002, 08:37:54 ; Search time 102.05 Seconds (without alignments) 103.575 Million cell updates/sec
                                                                                                                                                                                                                           US-09-674-857-7
583
1 APEFLGGPSVFLFPPRPKDT......CKVSNKGLPSSIEKTISKAK 110
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                         OM protein - protein search, using sw model
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Perfect score:
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283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Sequence:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 4 3 2 1. .. Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length	DB	ID	Description
_	583	100.0	327	; ₋	G4HU	Iq qamma-4 chain C
٥,	551	94.5	234	7	PT0207	
_	551	94.5	255	4	S31866	Ig gamma-1 chain C
	551	94.5	330	П	СННО	Ig gamma-1 chain C
	551	94.5	374	7	869339	Ig heavy chain V r
	541	95.8	377	7	A60764	Ig gamma-3 chain C
_	541	92.8	377	~	A23511	Id gamma-3 chain C
_	528	90.6	289	٦	G3HUWI	Id damma-3 heavy c
_	528	90.6	326	٦	G2HU	Iq qamma-2 chain C
10	470	80.6	328	7	147160	Ig gamma 2b chain
_	470	90.6	328	7	147159	
12	465	79.8	277	7	147162	Ig gamma 4 chain c
_	444	76.2	328	7	147161	Ig gamma 3 chain c
	444	76.2	328	~	147158	Iq qamma 1 chain c
	443	76.0	323	٦	GHRB	Ig gamma chain Cr
	443	76.0	333	7	PS0018	Ig gamma-2b chain
_	437	75.0	329	7	G2GP	Iq qamma-2 chain C
18	436	74.8	308	7	C30554	Ig heavy chain C r
19	436	74.8	472	7	S31459	-
_	434	74.4	470	7	S22080	Ig heavy chain pre
_	416	71.4	329	1	G3MSC	Ig gamma-3 chain C
~	416	71.4	398	7	G3MSM	Iq qamma-3 chain C
_	409	70.2	327	7	S06611	Ig gamma-2 chain C
	407	8.69	329	7	S00847	Iq qamma-2c chain
25	405	69.5	324	Н	G1MS	Ig gamma-1 chain C
	405	69.5	393	Н	G1MSM	
_	405	69.5	444	7	PC4436	monoclonal antibod
_	403	69.1	335	П	G2MSAB	Iq qamma-2a chain
_	399	68.4	330	Н	G2MSA	

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61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

Ig gamma-2a chain Iq gamma-2a chain	Ig gamma-2b chain Ig gamma-2b chain	Ig gamma-1 chain C Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma heavy cha	Ig epsilon-chain -	Ig epsilon chain C	Ig gamma-1 chain C	Ig heavy chain pre	Ig epsilon chain C
G2MSAM S37483	G2MSBM G2MS11	PS0017 S40295	501321	PS0019	B30503	A30503	146732	136948	ЕННО	S14236	S04845	EHRT
7		0 0	~	~	~	~	7	~	П	7	~	Н
399 469	405	326	475	322	112	88	180	426	428	152	549	429
68.4 68.4	68.3 68.3	66.7	62.9	58.8	53.3	47.7	44.3	28.7	28.6	28.3	26.4	25.9
399 399	398 398	389 389	384	343	311	278	258	167.5	166.5	165	154	151
30	32 33	34 35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1  Gyamma 4 chain C region - human  Cypecies: Homos sapiems (man)  Cypecies: Homos sapiems (man)  Cybecies: Homos sapiems (man)  Rillison, J.; Buxban, J.; Howd, L.  Notesion: Howolectide sequence of a human immunoglobulin C-gamma4 gene.  A.Reference number: A9033; MUD:03157104  A.Reference number: A9033; MUD:03157104  A.Reference number: A9033; MUD:03157104  A.Reference number: A9033  A.Rocesion: L.; Butterly. S.H.; De Vries, G.M.; Milstein, C.  Blochem. J. 117, 33-47, 1970  A; Title: Human immunoglobulin subiclasses. Partial amino acid sequence of the constant A; Reference number: A90249; MUD:70207560  A; Reference number: A90249; MUD:70207560  A; Rocession: An A90349  A; Rocession: A90	RESULT 1 G4HU Ig gamma-4 chain C region - human C;Species: Homo sapiens (man) C;Dactes: Homo sapiens (man) C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999 C;Accession: A90933; A90249; A02150 R;Ellison, J.; Buxbaum, J.; Hood, L.	DNA 1, 11-18, 1981 A; Title: Nuclectide sequence of a human immunoglobulin C-gamma4 gene. A; Reference number: A90933; MUID:83157104 A; Accession: A90933 A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-327 < ELL> A; Note: the sequence was determined from the germline gene B; Pink, J.R. D; Buttery, S.H.; De Vries, G.M.; Milstein, C.	A.Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant A; Reference number: A90249; MUID:70207560 A; Reference number: A90249; MUID:70207560 A; Rocession: A90249 A; Residues: 1-30; 81-326 <pin> C; Genetics: A; Genetics:</pin>	A;Introns: 99/1; 111/1; 221/1 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light ( C;Complex: An immunoglobulin heterotetramer subunit sand igh, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology cIMI>	F:134-20.3Domain: immunoglobulin homology <im2> F:134-20.3Domain: immunoglobulin homology <im3> F:240-107/Domain: immunoglobulin homology <im3> F:14/Disulfide bonds: interchain (to light chain) #status experimental F:27-83,141-201,247-305/Disulfide bonds: #status predicted F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F:17/Binding site: carbohydrate (Asn) (covalent) #status predicted</im3></im3></im2>	0%; Score 583; DB 1; Length 327; 0%; Pred. No. 1.1e-50; 0; Mismatches 0; Indels 0; Gaps
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A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:217370
The nucleotide
                                                                               A; Molecule type: DNA
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                                                  A; Accession: A93433
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C;Species: synthetic
G;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
G;Accession: S31866
B;Filpula, D.
Submitted to the EMBL Data Library, February 1993
A;Reference number: Sale66
A;Reference number: S31866
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                                                                          Jay Januara, Landran, C. Januara, C. Januara, C.; Species: Pan troglodytes (chimpanzee)
C; Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C; Accession: P70207
Mol: Immunol. 28, 319-322, 1991
A; Fitle: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Reference number: P70207; MUID:91287716
A; Reference number: P70207
A; Molecule type: mRNA
A; Residues: 1-234 *CERP>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species; Homo sapiens (man)
C; Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C; Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R; Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Nes. 10, 4071-4079, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
94.5%; Score 551; DB 2;
Best Local Similarity 93.6%; Pred. No. 1.1e-47;
Matches 103; Conservative 3; Mismatches 4
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3; Mismatches
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                                                             gamma chain C region - chimpanzee
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A; Residues: 1-255 <FIL>
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Matches 103; Conser
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A/Accession: B91006
A/Accession: B91007
A/Accession: B01007
A/Acce
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A; Residues: 2-330 < HAR>
A; Residues: 2-330 < HAR>
A; Cross-references: EMBL:21/370
B; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A; Tille: Structure of human immunoglobulin gamma genes: implications for evolution of A; Reference number: $33887; MUID:83001943
A; Accession: S33887.
                                                                                                                                                                                                                                                                                                                                A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 88-113; 235-330 <TAK>
A; Residues: 88-113; 235-330 <TAK>
A; Cossor-references: EMBL: 217370
B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma Biochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq A; Reference number: A90563; MUID:71064024
A; Contents: myeloma protein Eu
A; Accession: B90563
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A; Residues: 1-96, 'R', 98-135 <CUN>
A; Note: this sequence has the Gim(3) marker, 97-Arg
B; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
B; Cochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid s
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid s
A; Contents: E ago 56,4; MUID:71064025
A; Contents: E sequence has the Gim(non-1) markers, 239-Glu and 241-Met
A; Nonsting1, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A; Title: Die Primaerstruktur eines monoklonalen IgGl-Immunglobulins (Myelomprotein h
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238
                                                                                                                                                                                                                                                                                                                                                                               A; Note: Lys-330 is removed after translation R; Harris, L.J.
Submitted to the EMBL Data Library, October 1992 A; Accession: S38861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: B91668
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92.8%;
91.8%;
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Best Local Similarity 91.8%;
Matches 101; Conservative
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                                                                                                                                       A, Accession: A60764
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-377 <HUC>
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Best Local Similarity
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A; Residues: 1-377 <HUC>
          C; Accession: A60764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region precursor - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: S69339; #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S69339; #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S69339; #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S69339; Multiple of A.Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Reference number: S69339; Multiple of A; Status: preliminary
A; Molecule type: mRNA
A; Reference number: S7264
A; Residues: 1-140, CC, 142-374 < KH2>
A; Cross-references: EMBI: X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14923-33-14932.33
A:Map position: 14932-33-14932.33
A:Introns: 99/1; 114/1; 224/1
C:Comptex: An immunoglobulin heterotetramer subunit consists of two identical light (kinding all indumonoglobulin heterotetramer)
Discuperfamily: immunoglobulin c region; immunoglobulin homology
C:Superfamily: immunoglobulin c region; immunoglobulin homology
C:Reywords: duplication; 41ycoprotein; heterotetramer; immunoglobulin homology ciml>
F:20-69;Domain: immunoglobulin homology ciml>
F:37-310/Domain: immunoglobulin homology ciml>
F:37-310/Domain: immunoglobulin homology ciml>
F:27-81.14-204.250-308/Disulfide bonds: #status experimental
F:109.112/Disulfide bonds: interchain (to light chain) #status experimental
F:109.112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:109.112/Disulfide carbohydrate (Asn) (covalent) #status experimental
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C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 APELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 551; DB 1; Length 33
Pred. No. 1.7e-47;
3; Mismatches 4; Indels
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Pred. No. 2e-47;
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Best Local Similarity 93.6%;
Matches 103; Conservative
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Best Local Similarity 93.6
Matches 103; Conservative
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Best Local Similarity
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C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
A;Accession: A23511
                                                                                                                                c3, c5, u) with an IGHG4 conv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig gamma-3 heavy chain disease proteins - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999 C;Accession: A90442; A92219; A90198; A93315; A02149 R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C. Biochemistry 19, 4304-4308, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 377;
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A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: immunoglobulin C region; immunoglobulin homology
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R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl,
A;Reference number: A60764; MUID:90007613
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Pred. No. 2e-46;
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Pred. No. 2e-46;
3; Mismatches
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A;Cross-references: GDB:119339; OMIM:147120
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Jun 21

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A. Wolecule type: protein
A. Residues: 1-24, Fz. 76-75, Fy. 60-85;132-171, 7222',175, B',177-193, 'D',195-196,'Q',1
A. Wolecule type: protein
A. Residues: 1-24, Fz. 76-75, Fy. 60-85;132-171, 7222',175, B',177-193, 'D',195-196,'Q',1
A. Wole: this sequence has since been revised
A. Timunool. 16, 923-955, 1979
A. Timunool. 16, 923-955, 1979
A. Timunool. 16, 923-955, 1979
A. Accession: A93132
A. Accession: A93132
A. Accession: A93132
A. Molecule type: protein
A. Residues: 238-25 4609
A. Molecule type: protein
A. Residues: 238-25 4609
A. Molecule type: Alsa, Warch 1980
A. Molecule type: Alsa, March 1980
A. Mo
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A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Note: Trp-156 is at or near the complement-binding site
A; Note: Trp-16 is at or near the complement of the c
                                                                                                                                A)Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; PID:g6066056 A;Note: Lys-326 is probably removed posttranslationally R;Wang, A.C.; Tung, E.; Fudenberg, H.H. J. Immunol. 125, 1048-1054, 1980
                                                                                                                                                                                                                                                                                             A; Title: The primary structure of a human 19G2 heavy chain: genetic, evolutionary, A; Reference number: A92809; MUID: 81007873 A; Contents: myeloma protein Til A; Accession: A92809
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                                                                  A; Molecule type: DNA
A; Residues: 1-326 <ELL>
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                                                                                           A; Molecule type: mRNA
A; Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
C; Comment: The heavy chain disease protein Wis is shown.
C; Genetics:
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C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession. 3.3906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Froc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and Sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621
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A;Map position: 14q32.33-14q32.33
C. Superfamily: immunoglobulin c region; immunoglobulin homology
C;Superfamily: immunoglobulin c region; immunoglobulin; pyroglutamic acid
F;203-270,Domain: immunoglobulin homology <IMM>
F;203-270,Domain: immunoglobulin homology <IMM>
F;1,Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Pred. No. 2.9e-45;
6; Mismatches 6; Indels
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A;Contents: heavy chain disease protein Wis
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89.18;
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                                                                              A; Accession: A90442
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Matches 9
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                                                                        5 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE 64
   Length 326;
Score 528; DB 1;
Pred. No. 3.4e-45;
4; Mismatches 4;
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174

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Ig gamma 4 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: 147162

R;Racskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147163; MUID:95015845

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Rossion: 1277 < KAC>

A;Cross-references: EMBL:U03782; NID:9433129; PIDN:AAA52220.1; PID:9433130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47161
R;Racskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: I47158; MUID:95015845
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I41158
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A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 277;
                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: 1gC4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 465; DB 2;
; Pred. No. 5.5e-39;
12; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 444; DB 2;
Pred. No. 8.5e-37;
3; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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77.18;
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Best Local Simi
Matches 84;
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                                                                                                                  147160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofd domestica (domestic pig)
C;Date: 21.Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
R;Kacskovics, I;Sun, J;Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five.putative subclasses of swine IgG identified from the CDNA sequences of a A;Accession: 147160
A;Accession: 147160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <ARAC.
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma 2a chain constant region - pig (fragment)
C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Accession: 147159
B; Kacskovics, I.; Sun, J.; Butler, J.E.
J; Immunol: 153, 3565-3573 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A; Stetus: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Readidues: 1-328 < KAC>
A; Ctoss-references: EMBL: U03779; NID: 9433123; PIDN: AAA52217.1; PID: 9433124
A; Genetics:
A; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 133-202/Domain: immunoglobulin homology rIMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 GPSVFIFFPFKPKDTLMISTRPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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81.7%; Pred. No. 2.1e-39;
ive 12; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 470; DB 2;
; Pred. No. 2.1e-39;
12; Mismatches 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.6%; Score 470;
81.7%; Pred. No. 2
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Matches 8
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A. Residues: 1-323 < BER>
A. Wolecule type: mRNA
A. Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A. Reference number: A90290; MUID: 76135469
A. R. Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
B. Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
B. R. Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
A. Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A. Reference number: A93288; MUID: 83299917
A. Reference number: A93288; MUID: 83299917
A. Residues: 88-103, W.; 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 cMAR>
A. Residues: 88-103, W.; 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 cMAR>
A. Residues: GB: MI6426; NID: 9165111; PIDN: AAA31289 1; PID: 9165112
A. Note: this sequence has the dll allotypic marker, R.R. and the e15 allotypic marker Biochem J. 116, 249-259, 1970
A. Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin A. Reference in a number: A90245; MUID: 70110015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An *mmunoglobulin heterotetramer subunit consists of two identical light (kap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot
A;Reference number: A91749; MUID:84030930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 132-143, 'E', 145-161 <FRU>
R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A; Reference number: A94416
                                                                                                         ø
R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the CDNA sequences of A; Arleie: Five putative subclasses of swine IgG identified from the CDNA sequences A; Arleience number: I47158; MUID:95015845
A; Accession: I47158
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Wolecule type: mRNA
A; Residues: I-328 < KAC>
A; Coss references: EMBL:U03778; NID:9433121; PIDN:AAA52216.1; PID:9433122
C; Genetics:
A; Gene: IgGl
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 133-202/Domain: immunoglobulin homology < NMA>
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #Sequence_revision 15-Nov-1984 #text_change 16-Jul-1999
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 444; DB 2;
Pred. No. 8.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.2%;
77.1%;
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the subunits associate into
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hain disulfide bonds. In some cases, such as IgA and IgM, the subunits C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F; 20-82/Domain: immunoglobulin homology xIM2> F; 210-199/Domain: immunoglobulin homology xIM2> F; 236-303/Domain: immunoglobulin homology xIM2> F; 236-303/Domain: immunoglobulin homology xIM2> F; 236-303/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                        76.0%; Score 443; DB 1; Length 323; 74.3%; Pred. No. 1e-36; Live 11; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 81; Conserv
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Search completed: June 21, 2002, 08:37:54 Job time: 428 sec

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Sequence Sequence Sequence

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Sequence 30, Application US/08444644

Patent No. 601555
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESSONDENCES: 46
CORRESPONDENCES: 46
CORRESPONDENCES: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
        US-08-470-299-10
US-08-523-894-10
US-08-823-894-12
US-08-808-720-3
US-08-808-720-5
US-08-808-720-7
US-08-761-277A-45
US-09-485-7378-67
US-09-485-7378-67
US-08-232-539D-55
US-08-620-694A-4
US-08-633-639-4
US-08-630-633-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
APPLICATION NUMBER: ALK88-15AAAZ
FILING DATE: 07-SEP-1989
APPLICATION NUMBER: ALK88-15AAAZ
TELECOMMUNICATION NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617) 861-6540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                               US-09-022-696-4
US-09-022-253-4
                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
CITY: Lexington
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: INC
                                                                                                                                                                                                                                               US-08-444-644-30
June 21, 2002, 08:32:13; Search time 77.71 Seconds (without alignments) 34.261 Million cell updates/sec
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Sequence 30, Appl
Sequence 2, Appli
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Sequence 12,
Sequence 23,
Sequence 23,
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Sequence 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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                                                                                                                                  1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKTK
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                                                                                                                                                                                                                                                                                               Compugen Ltd
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US-08-23-246A-30

US-08-379-516-2

US-08-379-516-2

US-09-329-916-2

US-09-409-006A-2

US-09-409-006A-2

PCT-US-91-7460B-4

US-08-379-516-4

US-08-379-516-4

US-08-379-910-4

US-08-379-910-4

US-08-403-07422-4

US-09-39-910-4

US-09-39-910-4

US-09-403-07422-4

US-09-403-07422-4
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US-08-656-586-9
US-08-070-116A-4
US-08-232-246A-44
US-08-232-246A-44
US-08-761-277A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-470-299-7
PCT-US96-13152-4
US-08-704-744-81
US-07-916-098A-45
                                                                                                                                                                                                      hits satisfying chosen parameters:
          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                    231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                             US-09-674-857-2
580
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Match
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                                                                                                                                                       Scoring table:
                                                                                                                                     Sequence:
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1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                             1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                         61 REEQFNSTFRVVSVLIVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                     61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08477460B Patent No. 6034223 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 98.6%;
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                     US-08-477-460B-2
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Patent No. 6329508
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCES: 46
CORRESPONDENCES: Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                    1 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                           Score 572; DB 3; Length 109;
Pred. No. 6.1e-60;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 572; DB 4; Length 109;
Pred. No. 6.1e-60;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTARE: PC-DOS/MS-DOS SOFTARE: PC-DOS/MS-DOS SOFTARE: PC-DOS/MS-DOS SOFTARE: PC-DOS/MS-DOS SOFTARE: PC-DOS/MS-DOS SOFTARE: DS-DOS/MS-DOS SOFTARE: DS-DOS/MS-DOS SOFTARE: DS-DOS/MS-DOS SOFTARE: DS-DOS/MS-DOS SOFTARE: DS-DOS/MS-DOS SOFTARE: DS-DOS/MS-DOS SOFTARE: DS-DOS S
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REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.6%;
98.2%;
                                                                                                                                                        Query Match 98.6%;
Best Local Similarity 98.2%;
Matches 107; Conservative
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Best Local Similarity 98.2
Matches 107; Conservative
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internal
                                      internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-444-644-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02173
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-232-246A-30
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APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 572; DB 3; Length 43
Pred. No. 3.7e-59;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM TELECOMMUNICATION INFORMATION:
TELERPHONE: (212) 977-950
TELERAX: (212) 977-9809
TELEFAX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               OPERATING SISTEM: PC-LUCYMS-LUCS
SOCTHWARE: PALENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,460B
FILING DATE: 07-4UN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-40G-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
FEGISTRATION NUMBER: 28,678
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Gaps

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217 APPVAGPSVFLFPPKPKDTLAISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTXP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                      Score 572; DB 4; Length 432;
Pred. No. 3.7e-59;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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Patent No. 6187748

GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 07-UNW-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                        Query Match 98.6%;
Best Local Similarity 98.2%;
Matches 107; Conservative
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TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown MODECULE TYPE: protein ORIGINAL SOURCE: ORGANIC:
         TELERA: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 7
                                                                                                      LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 432 amino acids TYPE: amino acid
                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acidi
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                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
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                                                                                                                                                                                                                                                             CELL TYPE: lymphocyte US-09-329-916-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New COUNTRY: US. ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-485-372A-2
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US-08-3794516-2

Sequence 2, Application US/08379516

SEMERAL INFORMATION:

APPLICANT: Allaway, Graham P.

APPLICANT: Maddon, Paul B.

TITLE OF INVENTION: Immunoconjugates and Uses Thereof

TITLE OF INVENTION: Immunoconjugates and Uses Thereof

FILE REFERENCE: 41215-A-PCT-US

CURRENT APPLICATION NUMBER: US/08/379,516

SEARLIER APPLICATION NUMBER: DFT/US93/07422

SEARLIER PILING DATE: 1996-06-10

SEARLIER PILING DATE: 1992-08-07

NUMBER OF SEQ ID NOS: 9

SOCTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CQ4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.6%; Score 572; DB 3; Length 432; 98.2%; Pred. No. 3.7e-59; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
08/477,460
FILING DATE: 07-504-1995
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-6405-1992
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/329,916
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6177549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 98.29
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo saplens US-08-379-516-2
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US-09-329-916-2
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APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: C04-GAMMA2 AND C04-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                          277 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 325
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                                           61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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CURREWY APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Progenics Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9307422 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08477460B Patent No. 6034223 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
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PCT-US93-07422-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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PCT-US93-07422-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-477-460B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PERTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: C04-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
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                                                                                                                                                                                                                                            1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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                                                                                                                               Length 432;
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Pred. No. 3.7e-59;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                            61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                           Score 572; DB 4; Length 43
Pred. No. 3.7e-59;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-LUCS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION ATA:
PRIOR APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ 15 077-9550
TELESTAX: (212) 977-9809
TELEX: 42253 COOP UI
STENGRATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09409006A Patent No. 6342586
                                                                                                                            98.68;
98.28;
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98.2%;
                                                                                                                                                  Best Local Similarity 98.2
Matches 107; Conservative
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Best Local Similarity 98.2
Matches 107; Conservative
; CELL TYPE: lymphocyte US-08-485-372A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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US-09-409-006A-2
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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: New York
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                                                                                                                            Query Match
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Gaps

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Patent NO. 041.0.1.
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CQ4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
TITLE OF INVENTION: CQ4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                    1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                              Length 530;
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                                                                                                                                                                                                                                                                                                                                                              61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                        Score 572; DB 3; Length 53 Pred. No. 4.8e-59; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,460
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/09329916
; Patent No. 6177549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CADADRESSE: COOPER & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                Query Match 98.6%;
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 530 amino acids TYPE: amino acid
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                 TYPE: PRT; ORGANISM: Hômo sapiens
US-08-379-516-4
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US-09-329-916-4
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Patent No. 6083478
GENERAL INFORMATION:
APPLICANT: Allaway Graham P.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICANTON NUMBER: US/08/379,516
CURRENT FILING DATE: 1996-06-10
NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 4.8e-59;
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                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: PATCATION DATA:
APPLICATION NUMBER: US/08/477,460B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
APPLORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/COKET NUMBER: 41215-A-PCT/JPW/AJM
TELEPHONE: (212) 977-9550
TELEPAN: 422233 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SCOURME CHARACTERISTICS:
FENCINE CHARACTERISTICS:
FENCINE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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EARLIER FILING DATE: 1993-08-06
EARLIER PELLON NUMBER: 07/927,931
EARLIER FILING DATE: 1992-08-07
NUMBER OF SEQ ID NOS: 9
                                                                                   ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITX: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 98.2
Matches 107; Conservative
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) CELL TYPE: lymphocyte
US-08-477-4608-4
                                            NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: cloriginal Source:
                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                10112
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Sequence 4, Application US/09409006A
Patent No. 6342586
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application PC/TUS9307422
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION:
NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-Aug-1992
ATTORNEY/AGBNT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JFW/AJM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 572; DB 4;
Pred. No. 4.8e-59;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                             OFFWARE: Patentin Release #1.24
SOFFWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: USA ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 977-9550
TELEFAX: (212) 977-9809
TELEEX: 422523 COOP UI
TELEX: 422523 COOP UI
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.6%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.29
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; CELL TYPE: lymphocyte US-09-409-006A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                            US-09-409-006A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
PCT-US93-07422-4
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                                                                                   1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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                                                                                                                                          61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                 61 REEQPINSTERVUSVLTVVHODMLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                Sequence 4, Application US/08485372A
Fatent No. 6187748
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
ITILE OF INVENTION:
NUMBER OF SEQUENCES: 9
CORRESPONDENCE & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
  Pred. No. 4.8e-59;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 37690-II-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILLING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: White, John P. REGISTRATION NUMBER: 28,678
  98.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
Best Local Similarity 98.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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US-08-485-372A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 107; Conserv
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US-08-485-372A-4
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30 Rockefeller Plaza

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FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40, 378
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Best Local Similarity 97.28
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.6%; Score 572; DB 5; Length 530; 98.2%; Pred. No. 4.8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                APPLICATION NOTE:

FILING DATE:

CLASSIFICATION

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,931

FILING DATE:

ATORNEY/AGENT INFORMATION:

NAME: White, John P.

REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

TELEPATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

TELEPATION NUMBER: 42550

TELEPATION POR SEQ ID 00: 4:

SEQUENCE GHARACTERISTICS:

LENGTH: 530 amino acids

LENGTH: 530 amino acids

TYPE: amino acid

STRANDENESS: unknown

TOPOLOGY: unknown

TOPOLOGY: unknown
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Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE NUMBER OF SEQUENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCES: 15
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WinPatin (Genentech)
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Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: homo sapien
CELL TYPE: lymphocyte
PCT-US93-07422-4
                                                            ZIP: 10112
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: CDNA ORIGINAL SOURCE:
New York
New York
                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94080
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1 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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22-Jan-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 21, 2002, 08:32:14
Job time: 88 sec.
                                                                                                                                    P0987r1
                                                                                                                            REFERENCE DOCKET NUMBER: P098
TELECOMMUNICATION INFORMATION:
TELERAX: 415/252-1994
TELERAX: 415/552-981
TELERAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Sequence 7 Sequence 1 Sequence 2 Sequence

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GENERAL INCORDATION:
APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
APPLICANT: Ballon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
SPRIOR SEQ ID NOS: 104
SSQ ID NO SSQ ID NOS: 104
SSG ID NO 67
SSQ ID NO 67
SSD ID NO 67
SEQ ID NO 67
US-08-236-311-7

US-08-457-918-7

US-09-18-7

US-09-131-247-16

US-09-131-247-14

US-09-131-247-14

US-09-131-247-14

US-09-131-247-14

US-09-131-247-14

US-09-138-593A-8

PCT-US95-03866-12

PCT-US95-03866-12

PCT-US95-0386-14

PCT-US95-0386-14

PCT-US95-0386-14

PCT-US95-0386-14

US-08-397-411-7

US-08-397-411-7

US-08-458-516-13

US-08-678-23

US-08-678-23

US-08-678-23
                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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; Patent No. 6350860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.5%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: SYNTHETIC US-09-485-737B-67
   US-09-485-737B-67
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   FEATURE
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                                                                                                             June 21, 2002, 08:32:14; Search time 77.71 Seconds (without alignments) 34.575 Million cell updates/sec
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                                                                                                                                                                                                                  APPVAGGPSVFLFPPKPKDT.....CKVSNKGLPSSIEKTISKAK
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                                   Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-485-7378-90
US-08-444-21
US-08-232-5396-521
US-08-332-5396-55
US-08-633-4
US-08-633-4
US-08-634-4
US-09-022-255-4
US-09-022-253-4
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US-09-022-253-4
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US-09-131-247-6
US-08-284-391B-33
US-09-218-950-33
                                                                                                                                                                                                                                                                                                                                     hits satisfying chosen parameters:
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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US-09-022-257-4
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Maximum Match 100%
Listing first 45 summaries
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1 APPVAGGDSVETENT
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length: 2000000000
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fotal number Minimum DB Maximum DB

Database

Result Š.

Searched:

Seguence:

Run on:

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Sequence 90, Application US/09485737B
Patent No. 6350860
GENERAL INFORMATION:
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
                              ö
                                                                        Gaps
                                                          9
                                                         1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                             ö
                                                                                                                  Length 468;
Score 562; DB 4; Length 46
Pred. No. 1.4e-58;
2; Mismatches 3; Indels
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US-09-485-737B-90
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> Sequence Sequence Sequence

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Sequence Sequence

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US-08-459-657-43 US-08-460-132-43 US-08-466-465-8 PCT-US92-02050-43

US-09-180-100-11

-07-940-861-43 -08-459-512-43

US-09-178-869-4 US-09-178-869-2

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Wagner, Richard W
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COUNTRY: US
ZIP: 02173
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US-08-444-644-21
Sequence 21, Application US/08444644
Fatent No. 6015555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
FILE REFERENCE: INNS:015

CURRENT APPLICATION NUMBER: US/09/485,737B

CURRENT FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: PCT/FEP 98/05165

PRIOR PELING DATE: 1998-08-14

PRIOR PELING DATE: 1998-06-18

PRIOR PELING DATE: 1998-06-18

PRIOR PELING DATE: 1998-06-18

PRIOR PELING DATE: 1997-08-18

PRIOR PELING DATE: 1997-08-18

NUMBER OF SEQ ID NOS: 104

SOFTWARE: Patentin version 3.0

LENGTH: 711

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 562; DB 4; Length 711;
Pred. No. 2.5e-58;
2; Mismatches 3; Indels
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SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
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PRIGR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS NOT SOFTWARE: PA+****
CURRENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.7%;
Best Local Similarity 95.5%;
Matches 105; Conservative
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RESULT 4
US-08-232-346A-21
US-08-232-346A-21
Sequence 21, Application US/08232246A
Setent No. 6325908
GENERAL INFORMATION:
PAPLICANT: FIGHO, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Pred. No. 8e-59;
2; Mismatches 4; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

POFTWARE: Patentin Release #10, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/23,246A

FILING DATE: 04-MAY 1994

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: US 07/800,458

FILING DATE: 26-NOV-1991

PRIOR APPLICATION NUMBER: PCT/US90/05077

FILING DATE: 07-SEP-1990

PRIOR APPLICATION NUMBER: US 07/404,089

FILING DATE: 07-SEP-1990

PRIOR APPLICATION NUMBER: US 07/404,089

FILING DATE: 07-SEP-1989

ATPORNEY/AGENT INFORMATION:

NAME: Wagner, Richard W.

REGISTRATION NUMBER: 34,480

REGISTRATION NUMBER: 34,480

RELERANG (617) 861-6240

TELERANG (617) 861-6240

TELERANG (617) 861-6240

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 861-6240
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                 2. ....IRISTICS: .....IERISTICS: TYPE: amino acid TOPOLOGY: 1:-COLPOTTON TOPOLogy: 1:-COLPO
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94.58;
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Best Local Similarity 94.5
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-21
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                                                                                                                                                       DB 4; Length 110;
                                                                                                                                                                                          4; Indels
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COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
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94.9%; Score 557; DB 2;
Best Local Similarity 94.5%; Pred. No. 8.6e-59;
Matches 104; Conservative 2; Mismatches 4,
                                                                                                                                                   Score 557; DB 4;
Pred. No. 8e-59;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IGE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P0718P3
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 55, Application US/08232539D Patent No. 5965709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07.JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET UNMBER: POT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                     Query Match 94.9%;
Best Local Similarity 94.5%;
Matches 104; Conservative
 : 110 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 116 amino acids
Amino Acid
                                                        MOLECULE TYPE: protein FRAGMENT TYPE: internal
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                     TYPE: ami
TOPOLOGY:
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                                                                                              US-08-232-246A-21
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LENGTH:
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6 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 65
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                                                                                                                                                                                                                                                                            APPLICANT: COHEN, JEFFREY
APPLICANT: COMEAU, MICHAEL
APPLICANT: FARRAH, THERESA
APPLICANT: SPRIGGS, MELANIE
TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
TITLE OF INVENTION: That Bind MHC Class II Beta Chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                            PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.9%; Score 557; DB 1; Length 212; 94.5%; Pred. No. 1.9e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUFTWARE: Microsoft Word for Apple, Version 5.1a CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,633
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/235,397
FILING DATE: 04/28/94
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMUNEX CORPORATION
                                                                                                                                                                            Sequence 4, Application US/08430633
Patent No. 5726286
                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                           RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                       APPLICANT: ALDERSON, MARK
APPLICANT: ARMITAGE, RICHZ
APPLICANT: COHEN, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 212 amino acids
amino acid
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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CLONE: 19G1 FC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98101
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                       RESULT 6
US-08-430-633-4
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1 APPVAGGPSVFLFPPKPXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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APPLICANT: COMEN, JEFFEY
APPLICANT: COMEN, MICHAEL
APPLICANT: FARRAH, THERESA
APPLICANT: SPRIGGS, MELANIE
TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09022255
Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yeo, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Apple Operating System 7.1 SOFTWARE: Microsoft Word for Apple, Version 5.1a CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,854
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
94.9%; Score 557; DB 2;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICR APPLICATION: 430

PRICR APPLICATION NUMBER: US 08/430,633

FILING DATE: 28-APR-1995

APPLICATION NUMBER: US 08/235,397

FILING DATE: 04/28/94

ATTORNEY/AGENT INFORMATION:

NAME: PERKINS, PATICIA A.

REGISTRATION NUMBER: 34,693

REFERNENCE/DOCKET NUMBER: 2612

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEPHONE: (206)287-0430

TELEPHONE: CASO,233-0644

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 212 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                        ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                ARMITAGE, RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
CLONE: 19G1 FC
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-936-854-4
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APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.9%; Score 557; DB 2; Length 212; Best Local Similarity 94.5%; Pred. No. 1.9e-58; Matches 104; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION DATA: USA08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION BATA: APPLICATION WHERE: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERKIANS, PALTICIA ANDE
REGISTRATION UNMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
                               Sequence 4, Application US/08620694A Patent No. 5869286 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08936854
Patent No. 5925734
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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CLONE: 1961 FC
US-08-620-694A-4
JS-08-620-694A-4
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Gaps

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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206)587-0430
TELEFAX: (206).
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
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                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CLONE: ]
US-09-022-696-4
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Patent No. 6072037
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.9%; Score 557; DB 3; Length 212; 94.5%; Pred. No. 1.9e-58; tive 2; Mismatches 4; Indels
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FLING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2617-B
                               ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 94.59
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein ORIGINAL SOURCE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Co
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IMMEDIATE SOURCE:
CLONE: 1961 FC
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                                                                      Seattle
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                                                                                                              USA
                                                                                                            COUNTRY: U
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Sprigs, Metanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.9%; Score 557; DB 3; Length 212; Ilarity 94.5%; Pred. No. 1.9e-58; Conservative 2; Mismatches 4; Indels
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ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOSTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION NUMBER: US/09/022,696
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
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14 APELLGGPSVFLFPPFRFKDTLMISRTPEVTCVVVDVSHEDPEVFFNWYVDGVEVHNAKTK 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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MEDIUM TYPE: Floppy disk
COMBUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DAYS: US/09/022,259
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94.9%; Score 557; DB 3;
Best Local Similarity 94.5%; Pred. No. 1.9e-58;
Matches 104; Conservative 2; Mismatches 4
                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
RECISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US/09/022,260 FILING DATE:
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
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Patent No. 6191104
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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IMMEDIATE SOURCE:
CLONE: IGG1 FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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Petent No. 6100235
CEMERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 1.9e-58;
2; Mismatches 4; Indels
OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/022,253 FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
FILING DATE: 7 AUGUST 1995
FILING DATE: 7 AUGUST 1995
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acid
TYPE: amino acid
STRANDEDNESS: NO. 6096305 Relevant
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STREET: 51 University Street
CITY: Seattle
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Best Local Similarity 94.5%;
Matches 104; Conservative
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inmediate source:
CLONE: 19G1 FC
US-09-022-253-4
                                                                                                             CLASSIFICATION:
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US-09-022-260-4
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TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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MOLECULE TYPE: protein
US-08-595-043A-50
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; CLONE: 19G1 FC
US-09-022-257-4
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APPLICANT: Yea, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Stariow, William
APPLESED: INWENTON: No. 6197525el Receptor That Binds IL-17
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inmunex Corporation
STREET: 51 University Street
CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 212;
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Pred. No. 1.9e-58;
2; Mismatches 4;
PRIOR APPLICATION DATA:
APPLICATION UNBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFTCATION:
ATTORNEY/AGENT INFORMATION:
NAME: PERKATION NUMBER: 34.695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (206)587-0430
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
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                                                                                                                                                                                 TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.9%;
94.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.5'
Matches 104; Conservative
                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                              ; IMMEDIATE SOURCE:
; CLONE: 19G1 FC
US-09-022-259-4
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STATE: WA
COUNTRY:
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TCLASSITUATION:

ATCHASATION:
WANE: PERKINA, FABLICIA Anne
REGISTRATION UNDER: 34.635
REGISTRATION UNDER: 34.635
REGISTRATION UNDER: 34.635
REGISTRATION UNDER: 3.105
REGISTRATION UNDER: 3.11-8
REGISTRATION UNDER: 3.11-8
REGISTRATION UNDER: 3.12-8
RESIDENT: 3.12-8
RESULT 15
REGISTRATION UNDER: 30-13
REGISTRATI
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Query Match
94.9%; Score 557; DB 2; Length 232;
Best Local Similarity 94.5%; Pred. No. 2.2e-58;
Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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>1	⊣	APPVA	1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60	4ISRT	PEVTCVVVDVSHED	PEVK	FINAYVDGVEVE	INAKT	09 >	
۵	16	APELL(	16 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75	AISRT	PEVTCVVVDVSHED	PEVKI	NWYVDGVEVE	- AK	75	

¹⁶ APELLGGPSVFLEPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75

Search completed: June 21, 2002, 08:32:14 Job time: 88 sec

Human immunoglobul Native IgG Fc regi Native IgG Fc regi Human IgG Fc 1 all Human IgG Fc 1 all Human IgG1 non-A F Human IgG1 A allot Sequence of human Immunoglobulin G F

Human immunoglobul Fc region of human Fc region of human

Human 1961 Fc prot Human 1961 Fc chai Human 1961 Fc regi Human 1961 hinge/F

Human IgGgammal hi Human immunoglobul Human immunoglobul

Human immunoglobul Human partial 1961 Human 1969ammal hi Human immunoglobin

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Searched:

Database :

Perfect score:

Title:

Run on:

Sequence:

Scoring table:

Human Fc (1gd1).
Amino acid sequenc Human igG1 Fc regi Fc-MMP inhibitor f Fc-TMP protein seq TMP-Fc protein seq

FC-TNF-alpha inhib TNF-alpha inhibito FC-IL-1 antagonist IL-1 antagonist-FC MMP inhibitor-FC f

Humanised antibodies having modified allotypic determinant useful for matching allotypes in therapy with decreased likelihood of causing undesirable immune responses

WPI; 1992-349162/42.

Disclosure; Fig 4c; 57pp; English

Iggl Fc protein us Human IgGl Fc prot Human IgGl Fc regi

IgGl Fc regi

Human

AAY23637 AAW92411 AAY99937 AAY97182

997.3 997.3 997.3 997.3 997.3 997.3 997.3

572 572 572 572 572 572 572 572 573

Human immunoglobul Human IgGl Fc regi Human immunoqlobul

Query Match

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Isoallotype; IgG1 Glm(1,2,17); anti-allotype response; humanised Ab.
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AAY72915
AAB80897
AAB49155
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AAP82508
AAB16955
AAY96529
AAY96529
                                                                                                                  AAB76421
AAB76422
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AAY70251
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AAM50246
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AAB17954
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                                                                                                                                                                                                                                                                                                                                              AAY06617
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAB16961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunoglobulin IgG1 CH2 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR27680 standard; Protein; 110 AA
92WO-GB00445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91GB-0005245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LYNX-) LYNXVALE LTD
                                                                                                                                                                                                                                                     997.3
997.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09216562-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR27680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR27680
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
9: /SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
110: /SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
111: /SIDSI/gcgdata/hold-geneseqy-embl/AA1982.DAT:*
112: /SIDSI/gcgdata/hold-geneseqy-embl/AA1992.DAT:*
113: /SIDSI/gcgdata/hold-geneseqy-embl/AA1992.DAT:*
114: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
115: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
116: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
117: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
118: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
119: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
120: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
121: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
122: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
123: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
124: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
125: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
126: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
127: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IgG1 Fcgamma
Immunoglobulin G1
                                                                                               ; Search time 224.82 Seconds
(without alignments)
54.346 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunoglobul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDT......CKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                 747574
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                               hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                   747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR27680
AAR41684
AAY42621
AAR87023
AAR97264
AAW47354
                                                                                                  June 21, 2002, 08:36:09
                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A_Geneseq_032802:*
                                                                                                                                                          US-09-674-857-10
                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
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allergic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5965709-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                 AAY42621;
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAR41682-85 are encoded by the expression vector,
         In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17. The inventor's propose eliminating these allotypes by amino acid changes to agree with the sequences of 1gG2, 1gG3 and IgG4. None of the allotype sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes" should be suitable for therapeutic use in all patients. See AAR27678-R27681.
                                                                                                                                                      Gaps
                                                                                                                                                                                        Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                 Length 110;
                                                                                                                                                                                                                           PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                       2; Indels
                                                                                                                                Score 572; DB 13;
Pred. No. 4.9e-50;
                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 11K; 151pp; English.
                                                                                                                                                                                                                                                                                                         AAR41684 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                Undefined ORF2 encoded by pAH4602.
                                                                                                                               97.38;
97.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-0800458.
                                                                                                                            Query Match 97.3
Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ALKE-) ALKERMES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-196742/24.
                                                                                              110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ43844
                                                                                                                                                                                                                                                                                                                                                          20-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9310819-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Friden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
                                                                                                                                                                                                                                                                                                                                  AAR41684;
                                                                                             Sequence
                                                                                                                                                                                                                          61
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The invention provides immunoglobulin E (IgE) antagonists comprising one or more of the FeepsilonRI receptor-binding determinant sites of human ligE. The antagonists include IgE variants comprising an immunoglobulin template and binding determinant sequences (bds) CDbds, EFbds and the sequence shown in AAY42581. The CDbds (CD loop binding determinant sequence) are selected from the sequences shown in AAY42567 and the EFbds (EF loop binding determinant sequences are selected from sequences shown in AAY42578-Y42580. The variants are useful in raising and screening anti-IgE antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment and prophylaxis of allergic
gammal CH region CH at the 3' end of the VH-J region by means of a Nhel site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuro-pharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin E; IgE; antagonist; FoepsilonRI receptor; human; bds;
receptor-binding; binding determinant sequence; anti-IgE antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 572; DB 14;
Pred. No. 4.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4.9e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY42621 standard; protein; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.38;
97.38;
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94US-0178583
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.3
Best Local Similarity 97.3
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-579941/49.
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Sequence
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                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the human immunoglobulin G1 Fc region, and was used in creating a BZLF2-immunoglobulin Fc fusion protein (BZLF2/FC). BZLF2 is a Epstein-Barr virus (EBV) protein. To create BZLF2/FC, this sequence, the leader sequence of mouse interleukin-7 (IL-7) (see AAR87021), a Flag octapeptide (see AAR87022) and a flexible linker (see AAR87021) are joined to the extracellular domain (residues 34 to 223) of the BZLF2 sequence (see AAR87020). The BZLF2/Fc fusion protein containing this sequence is referred to in claim 4. BZLF2 proteins are members of the C-type lectin family. The C-type lectin domain is found in type II membrane proteins. The BZLF2 protein is capable of binding the beta chain of a major histocompatibility complex (MHC) class II antigen. Fusion proteins with an oligomerising zipper domain (OZD), instead of an immunoglobulin Fc region, can also be created. BZLF2
                                                                                                                                                                                                                                                                                                                           BZLF2; epstein-barr virus; EBV; C-type lectin; beta chain; MHC; antigen; major histocompatibility complex; immunoglobulin; cytotoxic T cell; autoimmune disease; myasthenia gravis; multiple sclerosis; allergy; systemic lupus erythematosus; organ transplant rejection; asthma; IL-7; tissue transplant rejection; therapy; cancer; viral disease; mouse;
                                                                               Gaps
                                                                                                      1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                  Epstein-Barr virus BZLF2 fusion proteins - used for treating e.g. auto-immune disease, transplant rejection, allergy, asthma, cancer
                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŢM;
                                                       Length 116;
                                                                                                                                                  61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                Farrah
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comeau MR,
                                                        DB 20;
                                               Score 572; DB 20,
                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cohen JI,
MK;
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                                                                                                                                                                                                                                AAR87023 standard; protein; 212
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) US NAT INST OF HEALTH.
                                                        97.3%;
97.3%;
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                                                                                                                                                                                                                                                                                                      Immunoglobulin G1 Fc region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Armitage RJ,
                                                                    Best_Local Similarity 97.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-393086/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viral infection
                        116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hutt-fletcher LM,
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9530015-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                       inteleukin-7
                                                                                                                                                                                                                                                                               11-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alderson M,
                        Sequence
diseases
                                                          Query Match
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(USSH
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proteins inhibit antigen-specific antibody formation, proliferation of blood monounclear cells and cytotoxic T cell responses. They also exhibit superantigen-like activity. The proteins can be used for treating or preventing autoimmune diseases such as myasthenia gravis, multiple sclerosis and systemic lupus erythematosus. Also, for treating organ or tissue transplant rejection and for treating or preventing allergy or asthma. They can be used for treating cancer and viral disease, especially EBV infection.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins - useful for treating rejection, allergy, asthma, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVS14; major histocompatibility complex; MHC; Class II; allergy, binding protein; inhibition; antigen presentation; superantigen; treatment; cancer; viral disease; immunoglobulin; IgG1; Fc region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which
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                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                               Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                  Score 572; DB 16;
Pred. No. 1.1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 32; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR97264 standard; protein; 212
                                                                                                                                                                                                                                                                                                                  97.3%;
97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US15948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0351901
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                                                                                                                                                                                                                                                                                                                                                                     Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alderson M, Armitage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated Herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-287183/29.
                                                                                                                                                                                                                                       212 AA;
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or viral disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral disease,
a superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9617939-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune
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Matches

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ð g RESULT AAW02305

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Epstein-Barr virus protein - binds to major histocompatibility complex class II beta chain, useful for treating, e.g. auto-immune diseases or transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence was used in the preparation of a synthetic construct containing the Epstein-barr virus (EBV) BZLF2 protein, which is capable of binding a beta-chain of a major histocompatibility complex (MHC) class II antigen. The protein can be used to inhibit antigen-specific antibody formation, peripheral blood mononuclear cell proliferation and cytotoxic T-cell responses, e.g. in the prevention or treatment of autoimmune diseases, transplant rejection, allergies or asthma,
                                                                                                                                               EBV; BZLF2; beta-chain; major histocompatibility complex; MHC; class II; antigen; prevention; treatment; autoimmune disease; transplant rejection; allergy; asthma; super-antigen; IgGl; Epstein-barr virus; human; immunoglobulin Gl; Fc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Comeau MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Columns 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         age RJ, Cohen JI,
Spriggs MK;
                                                                                                                 Human immunoglobulin G1 Fc fragment.
                     protein; 212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.38;
97.38;
                                                                                                                                                                                                                                                                                                                               95US-0430633.
                                                                                                                                                                                                                                                                                                                                                             95US-0430633.
94US-0235397.
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Armitage RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and as a super-antigen.
                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-192827/17.
                  AAW47354 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hutt-Fletcher LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 AA;
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                               28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                             28-APR-1995;
28-APR-1994;
                                                                                  01-JUN-1998
                                                                                                                                                                                                                                                              US5726286-A.
                                                                                                                                                                                                                                                                                              10-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                           Alderson M,
                                                  AAW47354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY23637;
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     AAW47354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The human IgG1 Fc region (AAW02305) can be used as a fusion partner for interleukin-17 receptor (IL-17R) proteins (see also AAW04184-85), allowing purification of recombinant IL-17R using protein A or protein G affinity chromatography. Fusions between Fc and HYS13 (see also AAW02387), a viral homologue of IL-17, and between Fc and murine CTLA8 (AAW02386) were used to identify cells that express the murine IL-17R. Selected murine thymoma EL4 cells were used as a source of murine IL-17R CDNA (AAT33800).
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                 9
                                                                               1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding interleukin-17 receptor - useful for regulating immune inflammatory responses, or to suppress graft rejection
                                                            1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
   Length 212;
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                                                                                                                            61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                               61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                 Indels
Score 572; DB 17;
Pred. No. 1.1e-49;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 572; DB 17;
Pred. No. 1.1e-49;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                       IgG1; interleukin-17 receptor; IL-17R.
                                                                                                                                                                                                                                          AAW02305 standard; Protein; 212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 33; 52pp; English.
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97.38;
97.38;
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97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0538765.
95US-0410535.
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                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.33
Matches 107; Conservative
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spriggs MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                          Human IgG1 Fc region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-443184/44.
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9629408-A1
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                         05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-1996.
                                 107;
Query Match
Best Local
                                                                                                                                                                                                                                                                         AAW02305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
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DNA

NAME OF COLOR OF STREET OF

Farrah TM;

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                                    Gaps
                                                                  1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                    ;
0
Length 212;
                                                                                                                                    61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                         IgG1 Fc protein used to make BZLF2 fusion proteins.
Score 572; DB 19;
Pred. No. 1.1e-49;
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RESULT

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us-09-674-857-10.rag

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10-JAN-2001
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23-MAR-1995;
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  US5869286-A.
                      09-FEB-1999
                                                            21-MAR-1996
                                                                      33-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY99937;
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY99937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                          The present sequence represents a protein used to create fusion proteins with the Epstein-Barr virus BZLF2 proteins of the invention. The BZLF2 protein is capable of binding to a beta chain of a class II major histocompatibility complex antigen to inhibit an antigen-specific response. BZLF2 is useful for inhibiting antigen-specific antibody and cytoxoic T cell responses. BZLF2 is also useful for inhibiting undestrable antigen specific responses, e.g. in the treatment or prevention of asthma; for preventing or treating autoimmune disease; and for preventing tissue or organ transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T cell proliferation; T cell activation; organ; graft; rejection; autoimmune disease; allergy; asthma; treatment; inflammatory disease; B cell proliferation; immunoglobulin secretion; immunogen; IgG1; Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor;
         BZLF2 protein; beta chain; blood mononuclear mononuclear cell; Class II major histocompatibility complex antigen; proliferation; cytotoxic I cell response; antigen specific response; asthma; autoimmune disease; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 572; DB 20; Length 212;
Pred. No. 1.1e-49;
1; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comeau MR,
                                                                                                                                                                                                  age RJ, Cohen JI,
Spriggs MK;
                                                                                                                                                                                                                                                                        Claim 2; Column 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                                                    Epstein-Barr virus BZLF2 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW92411 standard; Protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IgG1 Fc protein fragment.
                                                                                                                                         95US-0430633.
94US-0235397.
97US-0936854.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.3%;
Best Local Similarity 97.3%;
Matches 107; Conservative
                                                                                                                      97US-0936854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                      Armitage RJ,
                                                                                                                                                                                 (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                 WPI; 1999-418295/35.
                                                                                                                                                                                                    Alderson M, Armita
Hutt-Fletcher LM,
                                                            Homo sapiens
                                                                                                                      24-SEP-1997;
                                                                                                                                                   28-APR-1994;
24-SEP-1997;
                                                                            US5925734-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                          28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1999
                                                                                                 20-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW92411;
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This sequence represents a human IgG1 Fc fragment which is used in the construction of a fusion protein with human interleukin-17 receptor (IL-17R). IL-17R polypeptides have immunoregulatory activity. They can be used for inhibiting T cell proliferation, or for inhibiting T cell activation. In particular they can be used for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. They can also be used for the prevention or treatment of inflammatory disease in which activated T cells play a role or for inhibiting B cell poliferation or immunogalbullan secretion. The IL-17 polypeptides can also be used as immunogens, reagents in in vitro assays, or as binding agents for affinity purification procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated interleukin-17 receptor DNA - used to develop products for treating e.g. organ or graft rejection, autoimmune disease, allergy, asthma or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.3%; Score 572; DB 20; Best Local Similarity 97.3%; Pred. No. 1.1e-49; Matches 107; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Column 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; antibody; immune suppression
                                                                                                                                                                                                                                          2;
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                                                       96US-0620694.
95US-0410535.
95US-0538765.
   96US-0620694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                          Spriggs MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IgG1 Fc region.
                                                                                                                                                                               (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                     WPI; 1999-152766/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AA;
                                                                                                                                                                                                                                          Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
21-MAR-1996;
                                                                                                                     07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-1998;
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(IMMV ) IMMUNEX CORP.
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                          Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY97250;
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a novel receptor that binds Interleukin [27] [11-17, also known as CTLA-8] and a Herpesvirus saimiri homolog, HVS13. The receptor is a type I transmembrane protein which is referred to as IL-17R. Murine thymona El4 cells were found to express a receptor for IL-17. An EL4 mammalian expression library was screened and cDNA encoding the receptor was identified (see AAA6L238). The CDNA was used to isolate DNA encoding human IL-17R by cross species hybridisation. The human IL-17R cDNA and protein are described in that may be used with IL-17R cDNA and protein. Soluble forms of the receptor may be used to regulate immune responses, for example to support and accomponents of organ grafts. Antibodies to IL-17R consisting of amino acids 1-322 of murine IL-17R or 1-320 of human IL-17R may be used used in affinity purification of the receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri;
HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic;
anti-asthmatic; immunoglobulin G1; Fc region.
                                                                                      Antibodies immunoreactive with interleukin-17 receptor protein useful in interfering with receptor binding to CTLA-8, as components of diagnostic or research assays or in affinity purification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                               14 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktk 73
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                       97.3%; Score 572; DB 21; Length 212; 97.3%; Pred. No. 1.1e-49; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY97182 standard; Protein; 212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunoglobulin G1 Fc region.
                                              Yao
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95US-0410535.
95US-0538765.
 95us-0538765.
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                           Spriggs MK,
                      (IMMV ) IMMUNEX CORP.
                                                                  WPI; 2000-411206/35.
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
07-AUG-1995;
                                           Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-1998;
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23 - MAR-1995;
07 - AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                             107;
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                                                                                                                                                                                                                                                                                                                                                       Sequence
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Best Local S
Matches 107
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coby library from T cell thymoma EL4 cells, which were identified as coby library from T cell thymoma EL4 cells, which were identified as binding fusion proteins comprising human immunoglobulin G1 (19G1) Fc region and soluble LL-17 (CTLA-8) protein or a homologous Herpesvirus salmiri (HSV) protein, designated HSV13. Suppressing rejection of a grafted syngemeic or allogeneic organ or tissue in a graft recipient involves transfecting the organ or tissue to be transplanted with DNA encoding soluble IL-17R, so that expression of IL-17R by the current comprise residues 1-322 of the murine IL-17R, residues IL-17R fragments comprise residues 1-322 of the murine IL-17R, residues that bind IL-17. The method is useful for regulating an immunoresponse, for suppressing rejection of grafted organs or tissues in the recipient contributing diseases like allergy, asthma and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or
                                                                                                                                                                             Suppressing rejection of a grafted syngeneic or allogeneic organ tissue in a graft recipient for organ transplantation involves transfecting the organ or tissue with DNA encoding soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.3%; Score 572; DB 21;
97.3%; Pred. No. 1.1e-49;
live 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                       Example 1; Column 31-32; 27pp; English.
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                                                            Yao Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0620694.
95US-0410535.
95US-0538765.
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                                                         Spriggs MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.3'
Best Local Similarity 97.3'
Matches 107; Conservative
                                                                                                                                                                                                                                                                          interleukin-17R receptor
(IMMV ) IMMUNEX CORP.
                                                                                                                   WPI; 2000-523862/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases.
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23-MAR-1995;
07-AUG-1995;
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allergy or asthma in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                               AAB62062;
                                                                                                                                                                                      Seguence
 disease,
                                                                                                                                                                                                                                                                                                                                                       RESULT 1
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                                                                                                A novel interleukin-17 receptor (IL-17R) was identified by screening a binding fusion proteins comprising human immunospiobulin (1 (1961) FC region and soluble IL-17 (CTLA-8) protein or a homologous Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an Hamunos or inflammatory response in a mammal comprises administering soluble IL-17R. Soluble IL-17R fragments comprise residues 1-320 of the murine IL-17R, and fragments comprise residues 1-320 of the an immunoresponse, for treating or preventing diseases like allergy, asthma and autoimmune diseases, and for suppressing rejection of grafted organs or tissues in the recipient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-17 receptor; IL-17R; CTLA8; antiinflammatory; antiallergic; immunosuppressive; organ rejection; graft rejection; autoimmune disease; allergy; asthma; IgG1; immunoglobulin G1; human.
                                          Ø
                                     Regulating, treating or preventing immune or inflammatory response in mammal, especially organ or graft rejection, allergy or asthma, comprises administering interleukin-17 receptors
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                       14 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktk 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-17 receptor protein useful for regulating immune functio and for preventing or treating organ or graft rejection, autoimmune
                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                    Length 212;
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                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                    Score 572; DB 21;
Pred. No. 1.1e-49;
                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                Example 1; Column 31-32; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region of human immunoglobulin Gl.
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAB03809 standard; Protein; 212
 Yao
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                                                                                                                                                                                                                                                                   97.3%;
ilarity 97.3%;
Conservative
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95US-0538765
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Spriggs MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spriggs MK,
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                   WPI; 2000-548298/50
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                       212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-1996;
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Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1995
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB03809;
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This invention relates to an isolated and purified interleukin-17 receptor (IL-17R). A soluble IL-17 protein (CTLAB) and a herpesvirus similar (HVS13) open reading frame (homologous to CTLAB) were expressed as fusion proteins comprising an immunoglobulin Fc region, and used to screen for the expression of the IL-17R. The screening identified the novel receptor of the invention. IL-17R is a type I transmembrane protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic and antiallergic activities, and is an inhibitor of rell proliferation and activation. IL-17R can be used to regulate immune functions, and is useful for preventing or treating organ or graff rejection, autoimmune disease, allergy or asthma. The present sequence represents the Fc region of human immunoglobulin GI (19G1). This fragment of IgG1 forms part of the IL-17 fusion protein used to identify IL-17R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New assay kits for detecting interleukin-17 (IL-17), IL-17 receptors and (antagonists or mimetics of) the interaction between IL-17 and IL-17 receptor, useful for treating autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTLA-8; interleukin-17; IL-17; IL-17 receptor; IL-17R; human; IgG1; immunosuppressive; antiallergic; antiasthmatic; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 572; DB 21;
Pred. No. 1.1e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fc region of human immunoglobulin IgGl.
Example 1; Column 31-32; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.3%;
97.3%;
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95US-0410535.
95US-0538765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Interleukin-17 receptor; IL-17R; immunosuppressive; antiallergic; antiasthmatic; antiinflammatory; graft rejection; autoimmune disease; inflammatory disease; allergy; CTLA-8; immunogen; immunoglobulin G; IgG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the Fc region of human immunoglobulin IgG1 receptor (IL-17R).

The invention relates to Interleukin-17 receptors (IL-17R).

Interleukin-17 and their corresponding nucleic acid molecules. IL-17R is 4.7Ppe I transmembrane protein which is used for regulating the immune response. The invention is useful for suppressing rejection of a grafted organ or tissue in a graft recipient. Soluble IL-17 (CTLA-8) receptors are useful for preventing or treating organ or graft rejection,
interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R protein and a detecting reagent. The method is useful for inhibiting binding of IL-17 to cells expressing IL-17R. IL-17 receptors are also useful for preventing or treating organ or graft rejection, autoimmune diseases, allergy, asthma and inflammatory diseases in which activated T-cells play an important role. The present sequence represents For a property of human immunoglobulin IgG1, used for constructing a murine
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                  1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                   Suppressing rejection of grafted organ or tissue in graft recipient, involves administering to recipient a composition comprising interleukin 17 receptor protein -
                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                    Score 572; DB 22; Length 212;
Pred. No. 1.1e-49;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunoglobulin IgG1 Fc region
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                                                                                                                                                                                                    97.3%;
97.3%;
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95US-0410535.
95US-0538765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                               Query Match 97.3
Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                  CTLA-8/Fc fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fanslow WC;
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                                                                                                                                                   212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6191104-B1
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996k68 homo sapien
996kk8 homo sapien
096kk0 homo sapien
09brv0 homo sapien
09lz07 mus musculu
099ka4 mus musculu
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Hu Z., Garen A.;

"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";

Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

EMBL; AF272774; AAK586866.1;

EMBL; AF272774; AAK586866.1;

SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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97.3%; Score 572; DB 4; Length 701;
Best Local Similarity 97.3%; Pred. No. 1.8e-54;
Matches 107; Conservative 1; Mismatches 2; Indels
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9 SVFLFPPRPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                           Length 437;
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                                                                                                                                                                                           69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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Last annotation update)
                                                                             12;
                                   69.9%; Score 411; DB 11; 70.6%; Pred. No. 5.5e-37; ive 18; Mismatches 12;
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                                 Query Match
Best Local Similarity 70.6%
Matches 72; Conservative
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Best Local Similarity 70.6%
Matches 72; Conservative
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SEQUENCE FROM N.A.
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Q9D8L4;
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

T "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal

T antibody (Mab 7, its light and heavy chains) and construction of a

T single chain antibody (scFv)."

A Shmitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL, AR15372; AAA40243.1; -.

R EMBL, AR15372; AAA40243.1; -.

R EMBL, AR15372; AAA40243.1; -.

R InterPro; IPR003506; Ig_MHC.

DR InterPro; IPR003506; Ig_MHC.

DR PRART; SM00406; IGv; 1.

SMART; SM00410; IG_like; 2.

BR PRART; SM00410; IG_like; 2.

R PARRT; SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                     MEDLINE-98883416; PubMed-9717671; Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.; Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of commun. c-gamma, c-epsilon and c-alpha genes."; EMBL; AJ300675; CAC44624.1; -.
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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01-MAY'2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musines, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.8%; Score 469; DB 6; Length 33
75.5%; Pred. No. 1.6e-43;
tive 16; Mismatches 11; Indels
                                                                                                                                                                                                                                                          Wagner B.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
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Matches 83; Conservative
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                                                                                                                                     Equus caballus (Horse).
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SEQUENCE
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
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Matches 73; Conservative
                                                Best_Local Similarity 65.59
Matches 72; Conservative
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SEQUENCE FROM N.A.
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PROSITE; I
SEQUENCE
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              STRAIN-C57EL/G5. TISSUE-PANCREAS;

KRANINE-2108566): PubMed=11217851;

KRANINE-2108566): PubMed=11217851;

KRANINE-2108566): PubMed=11217851;

KRANINE-2108566): PubMed=11217851;

KRANINE SAILO T., CARLANI Y., KONDO H., Adachi J., Fukuda S.,

A AIZAWA K., IZAWA M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

KATO T., CARZAKI Y., Golobori T., Bono H., Kasukawa T., Saito R.,

KRAOCA K., Matsuda H.A., Ashburner M., Batalov S., Casuvant T.,

KRANINE R., Casuka H.A., Ashburner M., Eatalov S., Casuvant T.,

KRANINE R., Casuka H.A., Satuka H., Kondo H., Baldarelli R., Barsh G.,

Rochim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Rochone P., Marchdonni L., Mashima J., Mazzarelli J., Momberts P.,

KA, Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

KA, Marchdonni L., Mashima J., Mazzarelli J., Momberts P.,

KA, Sazaki H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mayashizaki Y.;

Thentional annotation of a full-length mouse cDNA collection.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; AAH10327.1; -.
Hypothetical protein.
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; PO1842; 7FAB.
MGD; MGI:96443; Igh-1.
InterPro; IPR003599; Ig_c1.
InterPro; IPR003609; Ig_like.
InterPro; IPR003606; Ig_like.
InterPro; IPR003606; Ig_MHC.
InterPro; IPR003596; Ig_NHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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  Length 473;
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                                                                                                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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$M004009; IG5, 2.
$M004006; IG4; 3.
$ $M00406; IG7; 1.
$; $M00410; IG_11Ke; 1.
$; $M00410; IG_11Ke; 1.
$ $F$00290; IG_MHC; UNKNOWN_1.

ITE; P$00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) SIMILAR TO RIKEN CDNA 1810060009 GENE.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
68.2%; Score 401; DB 11;
65.5%; Pred. No. 7.6e-36;
iive 18; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.5%; Score 397; DB 11; 66.4%; Pred. No. 2.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN 2001 (TrEMBLrel. 17, Created)
01-JUN 2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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09BU10;
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Q9BU10
          RESULT
Q9BQB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC
DDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VFLEPPKPRDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last sequence update)
HYPOTHETICAL 41.3 KDA PROTEIN.
HOMO Sapiens (Human).
BURATYOLE: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
24.1%; Score 142; DB 4; Length 375;
Best Local Similarity 28.7%; Pred. No. 1.9e-07;
Matches 29; Conservative 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004476.1; -.
R HSSP; P01857; 1FC1.
R InterPro: IPR003597; 1g_c1.
R InterPro: IPR003006; 1g_like.
R InterPro: IPR003006; 1g_MHC.
R Pfam; PF00047; 1g; 3.
R SMART; SM00410; 1G_like; 1.
R PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003596; Ig.V.
Pfam; PP00047; Ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00400; IGcl; 3.
SMART; SM00410; IG_like; 1.
SROUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
Strausberg R.; submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2001) to the EMBL, RECO03888; AAH03888.1; -. HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41314 MW; B1A0A0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.49
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=LYMPH, LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 375 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09BS21
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Q9BSZ1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 VFLFPPKPRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
Homo sapiens (Human).
Homo sapiens (Chuman).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-LIXE. LYMPHOMA;
Strausberg R.; LYMPHOMA;
Strausberg R.; LYMPHOMA;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002953; AAH02963.1; -.
HSSP; PO10825; FRAB.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Strausberg R.; Submitted (AAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006180; AAH01872.1; ...
                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | :: || :| || 426 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      597 AA
597 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=RHABDOMYOSARCOMA;
       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-LYMPHOMA;
                                                                                                                                                                                                                            NCBI_TaxID=9606;
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3

Gaps

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363 VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNAT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 67.8 KDA PROTEIN.
HYPOTHETICAL 67.8 KDA PROTEIN.
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.1%; Score 142; DB 4; Length 614; 28.7%; Pred. No. 3.5e-07; Live 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                 24.1%; Score 142; DB 4; Length 613; 28.7%; Pred. No. 3.5e-07; ive 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                         Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO1657; AAH11857.1;
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BCOGESI, AAH09951.1; -. SEF536E77AA9BBB CRC64; SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                         SEQUENCE FROM N.A.
TISSUE=PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN (PROTEIN FOR MGC:15420)
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SEQUENCE FROM N.A.
TISSUE-LYMPH, AND LYMPHOMA;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.78
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.15
Best Local Similarity 28.77
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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01-DEC-2001
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095626
1D 096636
AC 096636
DT 01-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096GA6
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Q96AA6
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (FOOTEIN FOR MGC:20337).
HOMO Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro: IPR003597; Ig_c1.
InterPro: IPR003606; Ig_like.
InterPro: IPR003606; Ig_like.
InterPro: IPR003506; Ig_like.
InterPro: IPR003596; Ig_w.
InterPro: IPR00405; Ig_ S.
InterPro: IPR00407; Ig_ S.
InterPro: IPR00406; Ig_ S.
InterPro: IRR00406; Ig_ S.
InterPro: I
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 WW; 4FCA3ADBECE263D9 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HOMPOTHETICAL 65.0 KDA PROTEIN.
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Matches 29; Conservative
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"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; allochemistry 9:3171-3181(1970).
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MEDLINE-82274238; PubMed-6287432;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
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MEDLINE-83289131; PubMed=6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin 1gG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-71064025; PubMed-5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
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Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
 P03988
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MEDLINE-17070269; PubMed=826475;
Ponstingl H., Hilschmann N.;
"The rule of antibody structure. The primary structure of
                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-GHG1.
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MUC_RABIT
MUCM_RABIT
                                              LAC_CHICK
HVC3_HETFR
                                                                            HVC1_HETFR
HVC2_HETFR
LAC1_MOUSE
ALC_MOUSE
                                                                                                                                        KAC4_RABIT
LAC5_MUSSP
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                                  MUC_CANFA
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Result Š. 

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GC2_HUMAN
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Blochemistry 20:2361-2370(1981).
--- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKER, 219-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER, 2 THE GIM (NON-1) MARKERS.
--- THE GIM (NON-1) MARKERS.
--- THE GIM (NON-1) MARKERS.
--- THE GIM (SOURCES HAVE THE GIM(3) S5,116,198,266,272.
--- THE CALLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF THE GIM (3) 155,166,177,195,198, 269, AND 272 AND IN THE ORDER OF RESIDUES
                                   MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Breie of antibody structure. The primary structure of a monoclonal 19G1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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InterPro: IPR0013006; Ig_MHC.
InterPro: IPR0013600; Ig_Cl.
InterPro: IPR0013600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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/FIId-vAR_003886.
D -> E (IN G1M(NON-1) MARKER).
FTId-vAR_003887.
L -> M (IN G1M(NON-1) MARKER).
/FIId-vAR_003888.
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REMOVED POST-TRANSLATIONALLY.
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                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; Pubmed-7236608;
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HINGE.
CH2.
CH3.
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Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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134
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PDB; 1FC1; 15-JUL-92.
PDB; 1FC2; 15-JUL-92.
                                                                                                                                     Deisenhofer J.;
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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2-326 FROM N.A. MEDLINE-82197621; PubMed-6804948; Ellison J.W., Hood L.E.; "Linkage and sequence homology of two human immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T., "Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982).
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                                                                                                                                                                   Length 330;
                                                                                Indels
   36106 MW; 3770EE106C2FA33D CRC64;
                                            Query Match 97.3%; Score 572; DB 1; L
Best Local Similarity 97.3%; Pred. No. 1.4e-50;
Matches 107; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-2 chain C region.
16HG2.
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MEDLINE-83001943; PubMed-6811139;
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330 AA;
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                       MEDLINE=84235992; PubMed=6329676; Krawinkel U., Rabbitts T.H.; "Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G., "Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";

Eur. J. Biochem. 228:886-893(1995).
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MEDIINE-80001357; Pubmed-113060;
Connell G.E., Parr D.M., Hofmann T.;
The amino acid sequences of the three heavy chain constant region domains of a human 1962 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
                                                                                                                                                                                                                                                                                                SEQUENCE OF 238-275 (21E).
MEDILINE-801141419, Pubmed-118920;
Hofmann T., Parr D. M.
"A note of the amino acid sequence of residues 381-391 of human
                                                                                                                     SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
MEDLINE-81007873; PubMed=6774012;
Wang A.-C., Tung E., Fudenberg H.H.;
"The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-69064124; PubMed-5782707;
Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
                                                                                                                                                                                                                                                                                                                                                                                                Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank
[3]
SEQUENCE OF 99-177 AND 310-326 FROM N.A.
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SEQUENCE OF 1-121 (DOT).
MEDLINE-95255298; PubMed-7737190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=72033500; PubMed=4940472;
                                                                                                                                                                                                                                                                                                                                                  immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J00230; AAB59393.1; -. PIR; A02148; G2HU. HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00290; IG_MHC; 2.
                                                                                              EMBO J. 1:403-407(1982).
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MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                             AT OR NEAR THE COMPLEMENT-BINDING SITE. REMOVED POST-TRANSLATIONALLY (PROBABLE)
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C -> S (IN REF. 3).
8310878CG878CF9C CRC64;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
BELINE-83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
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                                                                                                                                                                     CHAIN).
CHAIN).
                                                                                                                  INTERCHAIN (WITH A LIGHT CHAIN).
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Pred. No. 3.3e-48;
4; Mismatches 2;
         Immunoglobulin C region.
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1GHG4.
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PIR; A02150; G4HU.
HSSP; P01842; 7FAB.
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Immunoglobulin domain;
NON_TER 1 1
DOMAIN 1 98
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Best Local Similarity
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P01861;
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Matches
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GC4_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE-81021548; PubMed-6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
"Primary structure of human gamma 3 immunoglobulin deletion mutant:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Washaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 12-97 OF PROTEIN WIS.
MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Franglone B., Franklin E.C.;
Mrimary structure of the 'hinge' region of human 19G3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Blol. Chem. 252:883-889(1977).
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last amoncation update)
1g gamma - Schin C region (Heavy chain disease protein) (HDC).
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Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
The amino acid sequence of 'heavy chain disease' protein 2UC.
Structure of the Fc fragment of immunoqlobulin G3.";
Bicchem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                    INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                      (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 539; DB 1; Length 327; Pred. No. 3e-47;
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                                                                                                                                                                                                                                                                                                                                                                                  35940 MW; 3EDBD811EF208E7A CRC64;
                                                                                                                                                    Immunoglobulin C region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
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MEDLINE-82247835; PubMed-6808505;
                                                                                                                                                                                                                                                                                                      INTERCHAIN
            InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                        91.7%;
91.8%;
                                                                                                                              PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immun
NON_TER 1 1
DOMAIN 1 98
                                                                      Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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                                                                                                                                                                                                                                                                                                                                        141
247
327 AA;
MIM; 147130;
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P01860;
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GC3_HUMAN
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                                                                                                                                                                                                                                           Immunoglobulin C region; Glycoprotein; Repeat.
                                                                                           Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.

-!- MISCELLANEOUS: THE HENYY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                     GAMMA-3 HEAVY CHAINS.
-!- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
                                                                                                                                                                                                                                                                                                                                                                                                                   OR ANOTHER GAMMA CHAIN SUBCLASS.
-!- MISCELARROUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
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Alexander A., Steinmetz M., Barritault D., Frangione B., Franklin E.C., Hood L., Buxbaum J.N.; "Gamma Heavy chain disease in man: cDNA sequence supports partial
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N-LINKED (GLCNAC. . . ).
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/FICH=VAR_003890.

/FICH=VAR_003891.

F -> Y (IN OMM).

F -> Y (IN OMM).

T -> A (IN OMM).

T -> A (IN OMM).

/FICH=VAR_003892.
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InterPro: IPR003597; Ig_c1.
InterPro: IPR003600; Ig_like.
Pfam; PF00047; Ig_ 2.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunogl
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HSSP; P01857; 1FC1.
MIM; 147120; -.
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Brueggemann M.;

Brolution of the rat immunoglobulin gamma heavy-chain gene family.";

Gene 74.473-482(1988).

PIR. PSO018; PSO018.

HSSP; P01842; 7FAB.

HSSP; P01842; 7FAB.

InterPro; IPR003060; Ig_MHC.

InterPro; IPR003600; Ig_like.

InterPro; IPR003600; Ig_like.

PFam; PS000410; Ig_like; 1.

SWART; SW00407; IGG1; 2.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                            14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVQVHNAKTK 133
                                                                                                                                                                                                                                                                      Gaps
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Bukaryota; Metalos, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                          /FTIG-VAR_003895.
F -> Y (IN OMM).
/FTIG-VAR_003896.
E69CBC95705B2F46 CRC64;
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                                                                                                                                                                                                                       90.8%; Score 534; DB 1;
89.1%; Pred. No. 8.5e-47;
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       S -> N (IN OMM).
/FTId-VAR_003894
MISSING (IN ZUC).
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10-FEB-1991 (Rel. 17, Last sequence update)
10-FUL-1999 (Rel. 38, Last annotation update)
1g gamma-2B chain C region.
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MEDLINE-89232738; PubMed-3149946;
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Rattus norvegicus (Rat)
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Best Local Similarity
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Best Local Similarity
Matches 77; Conserv
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P20761;
VARIÀNT
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                                                                                                                                                                                                                                  Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                                                                                                                                                                                                                                       rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1- MISCELLANBOOS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKERS AND REF.5 THE E15 MARKER.
                                                                                                                Oryctolagus cuniculus (Rabbit).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
(Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 132-161.

MEDLINE-70110015; PubMed-5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-83299917; PubMed-6193512; M., Hood L., Knight K.L.; Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.; Heavy chain genes of rabbit 1965 isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes."; Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                     of the Fd sections of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> M (IN D11 MARKER).
-> A (IN E15 MARKER).
-> E (IN REF. 2).
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                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g gamma chain C region.
                     323 AA.
                                                                                                                                                                                                                                                                                                                                                  Pratt D.M., Mole L.E.;
"Sequence studies on the constant region of
immunoglobulin G of different allotype.";
Blochem. J. 151:337-49(1975).
                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=84030930; PubMed=6313520;
                                                                                                                                                                                                                                                                                                                                      MEDLINE-76135469; PubMed-1243651;
                                                                                                                                                                                                                                                                                     Immunogenetics 18:387-397(1983)
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HSSP; P01857; IFC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 88-266 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M16426; AAA31289.1; -.
                   STANDARD;
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SMART; SM00407; IGc1; 2.
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185
48
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185
48
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               GC_RABIT
P01870;
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CONFLICT
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VARIANT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                            Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED GUINEA PIGS.
                                                                                              Oliveira B., Lamm M.E.; ^{\circ} "Interchain disulfide bridges of guinea pig gamma-2-inmunoglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 PENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-88027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

NON. TER 1 1 1 1 INTERCHAIN (WITH A LIGHT CHAIN)

DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                        HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                        HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.1%; Score 436; DB 1; Length 32 74.3%; Pred. No. 7.6e-37; ive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 RVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36074 MW; 5D231B7164D1FBA9 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
19 gamma-3 chain C region, secreted form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 AA
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                                                            DISULFIDE BONDS.
MEDLINE=71058474; Pubmed=4922544;
                          iochemistry 13:4804-4811(1974).
                                                                                                                                                                            PIR, A02151; G2GP.
HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
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Best Local Similarity 74.39
Matches 81; Conservative
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79
105
107
110
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P22436;
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ID GC3_M
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the carboxyl-terminal
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"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                        PPVAGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
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BEDLINE-5036073. PubMed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 134-226.
MEDLINE-7036072. PubMed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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Pred. No. 7.5e-37;
3; Mismatches 17; Indels
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          2).
AND 4).
                                                            AND 5).
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69E8AA118D579A8B CRC64;
       V -> VPV (IN REF. 2).

V -> E (IN REF. 3 AND

V -> E (IN REF. 5).

V -> E (IN REF. 5).

V -> D (IN REF. 5).

V -> M (IN REF. 5).

V -> M (IN REF. 5).
REF. .
F. 3 A.
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"Structure of heavy chain from strain 13 guinea immunoglobulin-(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GC2_CAVPO STANDARD; PRT; 329 AA. 10186.186 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 gamma-2 chain C region.
                                                                                                                                                                                                                                                                                                                  13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trischmann T.M.;
Submitted (APR-1975) to the PIR data bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 4-68.
MEDLINE=71058471; PubMed=5538606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3iochemistry 13:4796-4803(1974).
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                                                                                                                                                                                                                                   MW.
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     71
144
1187
1187
201
201
246
256
256
266
280
35404
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       71
144
1173
1173
1201
231
246
256
266
266
280
323 AA;
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Best Local Similarity
Matches 79; Conserv
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CONFLICT
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GC2_CAVPO
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GC1_MOUSE
P01868;
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DOMAIN
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                             Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; Pubmed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.6%; Score 433; DB 1; Length 32 71.2%; Pred. No. 1.5e-36; ive 14; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                 114 223 CH2.
224 327 CH3.
329 AA; 36228 MW; F45827174182BAD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-3 chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 AA
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Nucleic Acids Res. 11:6775-6785(1983).
                                                                                                                                                                                                                                                                                                                    CH1.
HINGE.
CH2.
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EMBL; J00451; -; NOT_ANNOTATED_CDS PIR; B02156; G3MSC.
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BERH; V01256; CAA24767.1; ALT_SEQ.
PIR; AQ2155; G3MSM.
HSSP; P01857; 1FC1.
                                                                        Interpro: IPR003006; Ig_MHC.
Interpro: IPR003597; Ig_c1.
Interpro: IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; Ig_like; 1.
SMART; SM00407; IG_Li 2.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.23
Matches 79; Conservative
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113
223
327
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                                                       HSSP; P01857;
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P03987;
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DOMAIN
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDLINE-80012837; PubMed=113776;
Rogers J., Clarke P., Salser W.;
Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-80202559; PubMed-6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                              Pfam: PF00047; 19; 3.
SMART: SW00410; IG_like; 1.
SMART: SW00407; IG_like; 1.
FROSITE: PS00290; IG_MC: 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 433; DB 1; Length 398;
Pred. No. 1.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                  16; Indels
                                                                                                                                                                                                              CH3.

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

E - G (IN REF. 2).

E - Y (IN REF. 2).

F - F (IN REF. 2).

W, CF7F264B50A41B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                             73.6%; Score 433, --
71.2%; Pred. No. 1.9e
tive 14; Mismatches
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                                                                                                                                                                   CH1.
HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE (MYELOMA PROTEIN MOPC 21).
MEDLINE-78242288; Pubmed-98524;
                                                                                                                                                                                                                                                                                                                  43929 MW;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                             Query Match 73.6%
Best Local Similarity 71.2%
Matches 79; Conservative
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1113
2223
327
362
398
342
388
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                                                                                                                                                                                                                                                                                                 388
398 AA;
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                             domain
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                DISULFIDE BONDS (MOPC 21).
MEDINE-73008889; PubMed-5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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              Evolution of immunoglobulin subclasses. Primary structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:96446; Igh.4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
Pfan: PF00047; ig, 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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-> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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/FTId=CAR_000055.
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70.6%; Pred. No. 2.5e-34;
iive 18; Mismatches 12;
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                              murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
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                                                                                                                                                                                                                                                                                                                EMBL; V00793; CAA24172.1; -...
EMBL; V00793; CAA24173.1; -...
EMBL; V00793; CAA24174.1; -...
EMBL; V00793; CAA24175.1; -...
EMBL; V00795; CAA24175.1; -...
EMBL; V00795; CAA24176.1; -...
EMBL; V00799; CAA24176.1; -...

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P01869;
21-JUL-1986 (Rel. 01, Created)
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324 AA;
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Best Local Similarity
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Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;

NuCleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEGMENT OF MU CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                   [2]
MEDLINE-82197626, PubMed-6804950;
MEDLINE-82197626, PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
"mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                               MEDLINE-80045036; PubMed=115593; PubMod=115593; Menjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.; "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; cell 26:19-27(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
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HINGE.
CH2.
CH3.
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HSSP; P01842; 7FAB.
MGD; MGI:96446; Igh-4.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR03597; Ig_C1.
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217
324
82
102
                                                                                                                                                                                                                                                                                                                               gamma 1 chain gene.";
Cell 18:559-568(1979).
Mus musculus (Mouse).
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                   NCBI_TaxID=10090;
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21-JUL-1986
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30-MAY-2000
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or send an email to license@isb-sib.ch).
                                                                                                                                                               Gaps
                                                                                                                                                   9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 68
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                          Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D., "Multiple differences between the nucleic acid sequences of the
                                                                                                                                 ;
 INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                             Length 393;
                                                                                                                                12; Indels
                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4CC88343B7AICE27 CRC64;
                                        N-LINKED (GLCNAC. . .).
                                                                                                                                                                                          69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                       IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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                                                                                                          69.9%; Score 411; DB 1;
70.6%; Pred. No. 3.1e-34;
iive 18; Mismatches 12;
                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g gamma-2A chain C region, B allele.
                                                                                                                                                                                                                                                                  335 AA
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PIR; A02153; G2MSAB.
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6;
MEDLINE-82037861; PubMed=6170065;
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                                                                               43386 MW;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
                                                                                                                     Local Similarity 70.6
nes 72; Conservative
                                                                                                                                                                                                                                                                  STANDARD;
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1107
1109
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3357
                                                244 3
340 3
358 3
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MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uningalistic of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic family.";
                                                                                                                                                                                                                                                                                                          119 APDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 178
                                                                                                                                                                                   Gaps
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MEDLINE-81076554; PubMed-6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                               1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Determination of the primary structure of a mouse gamma G2:
immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Biochem. 30:452-462(1972).
                                                                                                                                                                                                                                                                                                                                                                         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                Length 335;
                                                                                                                                                                                   19; Indels
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36596 MW; FA3382792CBB13C6 CRC64;
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                                                                                                                    Score 403; DB 1;
Pred. No. 1.7e-33;
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SEQUENCE FROM N.A.
MEDLINE-81223894; PubMed-6787604;
MLD R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 39, Last annotation update)
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Nucleic Acids Res. 9:1365-1381(1981).
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65.5%;
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Best Local Similarity
Thes 72; Conserve
                       335 AA;
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DISULFIDE BONDS.
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Query Match 68.29
Best Local Similarity 65.55
Matches 72; Conservative
                                                Nature 296:761-763(1982).
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-80081502; PubMed=117549;
Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
"Sequence of the cloned gene for the constant region of murine gamma Science 206:1303-1306(1979).
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (A ALLELE).
MEDULINE-80120716; PubMed=6766534;
Yamawaki-Kataoka T., Kataoka T., Takahashi N., Obata M., Honjo T.;
"Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from newborn nouse DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                           ; Score 401; DB 1; Length 330;
; Pred. No. 2.6e-33;
17; Mismatches 20; Indels
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B84361C5445A6864 CRC64;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (MPC 11).
MEDLINE-80081501; PubMed=117548;
Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
"Structure of the constant and 3' untranslated regions of amma 2b heavy chain messenger RNA.";
Science 206:1299-1303(1979).
                                                                                                                             Immunoglobulin domain; Immunoglobulin C region.
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Last annotation update)
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  entities requires a license agreement (St
or send an email to license@isb-sib.ch).
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                                              HSSP, P01842, 7FAB.
InterPro: IPR003006, Ig_MHC.
InterPro: IPR003597, Ig_c1.
InterPro: IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                MM;
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                                                                                                                                                                                                                                                           68.2%;
66.4%;
                            EMBL; V00798; CAA24178.1; -. PIR; A02152; G2MSA.
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                                                                                                                                                                                                                                                                     Similarity 66.4%
73; Conservative
                                                                                                                                                                                                                                36389
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Best Local Simi
Matches 73;
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P01866;
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SEQUENCE
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MEDLINE-94216359; PubMed-7512967;
MEDLINE-94216359; PubMed-7512967;
Kim H., Yamaquchi Y., Masuda K., Matsunaga C., Yamamoto K.,
Irimura T., Takahashi N., Kato K., Arata Y.;
"O-glycosylation in hinge region of mouse immunoglobulin G2b.";
"O-glycosylation in hinge region of mouse immunoglobulin G2b.";
J. Biol. Chem. 208:1245-12356(1994).
"INTEREMINED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
MODIFIED WITH 2 SIALIC ACID RESIDUES.
SEQUENCE FROM N.A. (B ALLELE).
MEDLINE-82173203; PubMed-6803173;
Ollo R., Rougeon F.,
Menuse immunoglobulin allotypes: post-duplication divergence of gamma 2a and gamma 2b chain genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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REMOVED POST-TRANSLATIONALLY (PROBABLE)
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1-JUL-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 gamma-2A chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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T -> A [IN B ALLELE].

M -> D [IN B ALLELE].

M -> I [IN B ALLELE].

L -> S [IN REF. 2 AND 3).

S -> P [IN REF. 2 AND 3).

I -> T [IN REF. 2 AND 3).

K 7D879662607C356E CRC64;
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HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                              MEDLINE-8222190; PubMed-6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Nakai S.
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
4C38138BFAED3FF0 CRC64;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cd.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig_ 3.
SWART; SM00410; IG_like; 1.
SWART; SM00407; IG_Like; 1.
Immunoglobulin domain, Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
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PIR; A02154; G2MSAM.
HSSP; P01857; 1FC1.
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Query Match 68.2%; Score 401; DB 1; Length 399; Best Local Similarity 66.4%; Pred. No. 3.2e-33; Matches 73; Conservative 17; Mismatches 20; Indels 0; Gaps

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1 APPVAGGPSVFLEPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWVVDGVEVHNAKTK 60

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61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110

Search completed: June 21, 2002, 09:00:26 Job time: 1450 sec

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19 gamma chain C r
19 gamma-1 chain C
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gramma-1 chain C region - synthetic C;Species: synthetic A;Note: Homo saptens (man) gene engineered and expressed in Escherichia coll C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000 C;Accession: S1866 K;Filpula, D. submitted to the EMBL Data Library, February 1993 A;Description: Screeing method for protein-protein interactions of cloned gene produc

61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110 

85

Ω q A; Cross-references: EMBL: X70421; NID: 933068; PIDN: CAA49866.1; PID: 933069

A, Accession: S31866 A, Molecule type: mRNA A, Residues: 1-255 <FIL>

C.Keywords: immunoglobulin F:1-22/Region: Escherichia coli outer membrane protein A precursor F:23-255/Region: human Ig gamma-1 chain C region

97.3%; Score 572; DB 4; Length 255;

Query Match

G2MSA G2MSAM

30   401   68.2   405   1 G2MSBM   19 gamma-2b   33   401   68.2   446   2 S37483   19 gamma-2b   33   401   68.2   444   1 G2MS11   19 gamma-2b   34   393   66.8   475   2 S01047   19 gamma-2b   35   391   66.8   475   2 S01021   19 gamma-1b   19 gamma-1b   36   392   66.2   322   2 S00047   19 gamma-1b   10 gamma-1b   19 gamma-1b   19 gamma-1b   10 gamma-1b	Ig gamma-2b chain Ig gamma-2b chain Ig gamma-2b chain Ig gamma-2c chain Ig gamma-2b chain Ig gamma-2b chain Ig gamma-2b chain Ig gamma-1chain Ig gamma-1chain Ig gamma-1chain Ig epsilon-chain Ig epsilon chain	ALIGNMENTS  nzee panzee) vision 23-Nov-1991 #text_change 16-Jul-1999 Oestberg, L. chimpanzee Fc and hinge regions. :91287716 region; immunoglobulin homology homology <imm></imm>	DB 2; Length 234; 2.6e-50; thes 2; Indels 0; Gaps 0; DVSHEDPEVKENWYUGGVEVHNAKTK 60
30 401 68.2 405 1 31 401 68.2 469 2 33 400 68.2 469 2 34 393 66.8 475 2 34 393 66.8 475 2 36 389 66.5 326 2 37 354 60.2 322 2 38 319 54.3 112 2 39 275 46.8 88 41 16.5 28.0 428 1 42 16.5 28.0 428 1 44 16.5 28.0 428 1 45 160 27.2 429 1 47 16.5 28.1 426 61 48 1177 30.1 152 2 48 16.5 28.1 426 61 49 16.5 28.0 428 1 40 16.5 28.0 428 1 41 16.1 27.4 549 2 42 16.5 28.1 426 61 44 16.5 28.0 428 1 45 160 27.2 429 1 46 11.7 800xtafa, Z.A.; MACCESSION: PT0207 A, MOLECULE TYPE: MOUSTAFA, MUID A, TILE: NUClEOTIGE SEQUENCE Of A, Reference number: PT0207 A, MOLECULE TYPE: MRNA A, Reference number: PT0207 A, MOLECULE TYPE: MRNA A, Reference numbor: MRNA A, Reference numbor: PT0207 A, MOLECULE TYPE: MRNA A, Residues: 1.234 CEHR> C, Superfamily: immunoglobulin F, 48-117/Domain: immunoglobulin F, 48-111/FPFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	GZMSBM 237483 CZMS11 SCO8451 SCO847 SCO1321 SCO132 SCO17 P	ALIGNMENTS nzee panzee) vision 23-Nov- Oestberg, L. chimpanzee Fc :91287716 region; immuno	Score 572; DB 2; Pred. No. 2.6e-50. 1; Mismatches :: IISRTPEVTCVVVDVSHEDP! IISRTPEVTCVVVDVSHEDP! IISRTPEVTCVVVDVSHEDP!
30 401 68.2 465 31 401 68.2 469 32 401 68.2 469 33 400 68.0 329 34 393 66.8 475 36 389 66.2 322 37 354 60.2 322 38 319 54.3 112 39 275 46.8 88 40 264 44.9 180 41 177 30.1 152 42 165.5 28.0 428 44 161 27.4 549 45 160.2 37.2 429 46 160.2 37.2 429 47 160.2 38.0 19004ptes (c. C.) pace 23.Nov-1991 #sequence C. Accession: PTO207 A. Firlich, P. H.; Moustafa, Z. Molecule type: mRNA A. Reference number: PTO207 A. A. Accession: B. A.	ноновововонон	mpa him him him him him him him him	38; 38; OTLM
30 401 68.2 31 401 68.2 32 401 68.2 33 400 68.0 34 393 66.8 36 391 66.5 36 391 66.5 37 354 60.2 37 354 60.2 37 354 60.2 37 354 60.2 37 354 60.2 37 364.3 39 275 44.9 40 167.5 28.1 42 165.5 28.0 44 161 27.4 44 161 27.4 45 160 27.2 REBULT 1 Cregio C.Species: Pan troglog C.Speci	469 469 324 474 475 326 326 112 115 115 426 428 428 428 428 428 428 428 428 428 428	n - chi ytes (c equence afa, Z. 332, 16 quence 0207; h lobulir ulin	97. y 97. rvative FPPKPKI
30 401 68 31 401 68 32 401 68 33 400 68 34 393 66 36 391 66 37 354 60 38 319 54 40 264 44 40 264 44 41 167 30 42 165.5 28 43 164.5 28 43 164.5 28 44 161 27 45 160 27 46 160 27 47 160 20 47 160 20 48 161 27 48 161 27 48 161 27 48 164.5 28 49 164.5 28 49 164.5 28 49 164.5 28 49 164.5 28 49 164.5 28 49 164.5 28 49 160 27 40 20 20 20 20 50 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 60 20 20 20 20 20 20 60 20 20 20 20 20 20 60 20 20 20 20 20 20 60 20 20 20 20 20 20 20 60 20 20 20 20 20 20 20 60 20 20 20 20 20 20 20 60 20 20 20 20 20 20 20 20 60 20 20 20 20 20 20 20 20 20 20 20 20 20	44408844489440 <b>4</b> 4	gio 10d #sc #sc 119- PT RA BEHR nog 10b mun	rit nse VFL
30 401 31 401 32 401 33 4 401 33 4 401 33 4 401 34 393 35 391 36 391 37 354 40 264 40 264 40 264 42 165.5 43 164.5 44 161 62 Species: Poronomy C. Species: Poronomy C. Species: Poronomy C. Accession: PT R. Ehrlich, P. H. R. Esuine: 1-2 A. Title: Nucleo A. Reference num F. Accession: PT A. Molecule type A. Residues: 1-2 C. Supwords: imm F. 48-117/Domain F. 48-117/Domain C. Supwords: imm F. 48-117/Domain F. 48-117/F. 4	8888888888888888888888888888	C re 1990 1990 0207 7 Mo 8 , 3 8 , 3 14 ide 0207 1 imm unog	mila Co GGPS
30 31 32 33 33 33 33 33 33 33 33 33 33 33 33	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	a chain es: Pan 23-Nov-23-Nov-25-Nov-25-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-26-Nov-	Match Local Si es 107; 1 APPVA 1     :
	01000000000000000000000000000000000000	RESULT PT0207 IQ Gammi C; Specio C; Date: C; Acces: R; Ehrlin Mol. Im Mol. Im A; Refer A; Resid A; Resid C; Super: C; Super: C; Super: C; Super:	Query Best   Match

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A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A;Reference number: A91723; MUID:83289131
A;Contents: Myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Recesidues: 1-96, R', 98-197, 'D',199-238, 'E',240, 'M',242-266, 'D',268-271, 'D',273-330 <
A;Residues: 1-96, R', 98-197, 'D',199-238, 'E',240, 'M',242-266, 'D',268-271, 'D',273-330 <
A;Note: this sequence has the Glm(3) and Glm(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A;Reference number: A90565; MUID:71064027
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Redchel, W; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267
A;Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S6939; S72664
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Reference number: S69339
A; Status: prealiminary
A; Accession: S6939
A; Status: prealiminary
A; Residues: 1-374 < KHA>
A; Residues: mRNA
A; Reference number: S72664
A; Status: prealiminary
A; Molecule type: mRNA
A; Status: prealiminary
A; Cross-references: EMBL:X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:1GRG1
A;Crosx-references: GDB:120085; OMIM:147100
A;Gene: Teferences: GDB:120085; OMIM:147100
A;Gene: Teferences: GDB:120085; OMIM:147100
A;Map position: 14632.33-14632.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
Anin disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into
C;Complex: An immunoglobulin heterotetramer; immunoglobulin
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Keywords: immunoglobulin homology <IMI>-
F;107-85,Domain: immunoglobulin homology <IMI>-
F;137-206,Domain: immunoglobulin homology <IMI>-
F;137-1206,Domain: immunoglobulin homology <IMI>-
F;137-1206,Domain: immunoglobulin homology <IMI>-
F;137-1206,Domain: immunoglobulin homology <IMI>-
F;137-1206,Domain: immunoglobulin homology <IMI>-
F;109,IIII (ide bonds: interchain (to light chain) #status experimental
F;109,IIIZ/Disulfide bonds: interchain (to heavy chain) #status experimental
F;109,IIIZ/Disulfide carbohydrate (Asn) (covalent) #status experimental
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Pred. No. 3.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.3%; Score 572; DB Best Local Similarity 97.3%; Pred. No. 3.9e Matches 107; Conservative 1; Mismatches
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A; Residues: 1-96, 'R', 98-135 <CUN>
A; Residues: 1-96, 'R', 98-135 <CUN>
A; Note: this sequence has the Glm(3) marker, 97-Arg
R; Note: Uningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 88-113;235-330 <TAK>
A; Residues: 88-113;235-330 <TAK>
A; Residues: 88-113;237-370
B; Cross-references: EMBL:21370
B; Cunningham, B.A.: Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B; Cunningham, B.A.: Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B; A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequent A; Reference number: A90563; MUID:71064024
A; Accession: B90563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Rolecule type: 1-34,'Q', 36-96,'K', 98-115,'Q', 117-197,'D', 199-238,'D', 240,'L', 242-268,'E', 27
A;Note: this sequence has the Glm(17) and Glm(1) markers
A;Note: this sequence has the Glm(17) and Glm(1) markers
B;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's, Z. Physiol. Chem. 364, 713-747, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Wolecule type: protein A.Rolecule type: 104, (7, 156-165, (2, 167-176, (2, 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, A.Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met R.Ponstingl, H.; Hilschmann, N. Hopper-Seyler, E. Physiol. Chem. 357, 1571-1604, 1976 A.Title: Die Primaerstruktur eines monoklonalen IgGl-Immunglobulins (Myelomprotein Nie),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, A;Note: Lys:330 is removed after translation R;Harris, L.J. submitted to the EMBL Data Library, October 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Bate: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A9343; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071,4079, 1982
                                                     Gaps
                                                                                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93433; MUID:82274238
A;Accession: A93433
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0
                                                                                                                                                                                                                                                                                                                          99 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148
                                                                                                                                                                                                                                                                            61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                 Indels
        Pred. No. 2.8e-50;
1; Mismatches 2;
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A;Contents: myeloma protein Nie
A;Accession: B91668
    97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross·references: EMBL:217370
        Best Local Similarity 97.3
Matches 107; Conservative
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A; Molecule type: protein inc.
A; Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',1
A; Molecule type: protein
A; Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',1
A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.M.
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli
A; Acontents: Zie
A; Molecule type: protein
A; Accession: A93132
A; Molecule type: protein
A; Molecule type: 238-275 <400>
A; Molecule type: protein
A; Molecule type: 249-250
A; Molecule type: 249-250
A; Molecule type: 249-250
A; Molecule to the Atlas, March 1980
A; Reference number: A94591
A; Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A; Note: the revised sequence differs from that shown in having 60-Ala and in the amid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 14q32.33-14q32.33 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and 264-268
60-Ala and in the amid
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                   ö
                                                                                                                                Rigitatein, C.; Frangione, B.
Bocchem. J. 121, 217-225, 1971
A; Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A; Reference number: A90253; MUID:72033500
A; Reference number: A90253; MUID:72033500
A; Rocontents: annotation; myeloma protein Sa, disulfide bonds
R; Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A; Title: Structural studies of immunoglobulin G.
A; Reference number: A9315; MUID:69064124
A; Contents: annotation; Sa, disulfide bonds
                       Gaps
                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                   ö
                                                                                                                                                                                                                                                 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                    221 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
                       4;
                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: The amino acid sequences of the A; Reference number: A90752; MUID:80001357 A; Contents: myeloma protein Zie
                   3;
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma-2 chain C region -
               103;
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                       Matches
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C; Species: Home saplens (man)
C; Date: 28 Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C; Accession: A23511
R; Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A; Title: Sequence of a human immunoqiobulin gamma 3 heavy chain constant region gene: A; Reference number: A23511; MUID:86148507
A; Accession: A23511
A; Molecule type: DNA
A; Residues: 1-377 <HUC>
A; Residues: 1-377 <HUC>
A; Cossereferences: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics: GB:G16G3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                    218 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267
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                                                                                     Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, A;Reference number: A60764; MUID:90007613
A;Accession: A60764; MUID:90007613
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Reywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homolowy <IMM>
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                                                                                     Score 572; DB 2;
Pred. No. 4.5e-50;
1; Mismatches 2
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Pred. No. 3e-48;
3; Mismatches
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20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
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93.6%;
                                                                                         97.38;
97.38;
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Best Local Similarity 93.6%;
Matches 103; Conservative
                                                                                                                            Best Local Similarity 97.3
Matches 107; Conservative
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Best Local Similarity
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C.Accession: A90442; A92219; A92195; A03149
R.Frangione, B.; Rosenwaser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A.Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea A; Reference number: A90442; MUID:81021548
A; Contents: heavy chain disease protein Wis
                                                                                61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                                  Ig gamma-3 heavy chain disease proteins - human
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Best Local Si
Matches 98;
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hain disulfide bonds. In some cases, such as IqA and IgM, the subunits associate into la S. Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C; 20.65/Domain: immunoglobulin homology <IMI>C; 20.65/Domain: immunoglobulin homology <IMI>C; 20.75/Domain: immunoglobulin homology <IMI>C; 219.30(C/Domain: immunoglobulin homology <IMI>C; 210.20(C/Domain: immunoglobulin homology <IMI

E; 21.20(C/Domain: immunoglobulin homology <IMI

E; 21.20(C/Domai
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A Molecule type: DNA

A Residues: 1-37 < FELLS

A Note: the sequence was determined from the germline gene

R; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant

A; Reference number: A90249; MUID:70207560
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A.Introns: 99/1; 111/1; 221/1
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C.Superfamily: immunoglobulin c region; immunoglobulin homology
C.Keywords: duplication: glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
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C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fil34-203/Domain: immunoglobulin homology <IM2>
Fil34-203/Domain: immunoglobulin homology <IM3>
Fil44/Disulfide bonds: interchain (to light chain) #status experimental
Fil34/Disulfide bonds: status predicted
Fil05,109/Disulfide bonds: status resperimental
Fil05,109/Disulfide bonds: interchain (to heavy chain) #status experimental
Fil77/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.3%; Score 548.5; DB 1; Length 326; 93.6%; Pred. No. 9e-48; .ive 4; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.7%; Score 539; DB 1; Length 327; 91.8%; Pred. No. 8.2e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: protein
A Residues: 1-30;81-326 <PIN>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 91.8 Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB: IGHG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103;
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Best Local S
Matches 103
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A. Molecule type: protein
A. Residues: 1-289 <FRA>
A. Nestein the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A. Note: the sequence of residues 42-76 was taken from the reference that follows
A. Note: the sequence of residues 42-76 was taken from the reference that follows
B. Michaelsen, T. E.; Frandione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A. Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat
A. Reference number: A92219; MUID:77118561
A. Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 12-97 <MIC>
A; Note: the hinge region in gamma-3 chains is about four times as long as in other ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alote: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in Riwolfenstein-Todel, C.; Franglone, B.; Prelli, F.; Franklin, E.C. Biophys. Res. Commun. 71, 907-914, 1976
A;Tile: The amino acid sequence of "heavy chain disease" protein zuc. Structure of the A;Reference number: A90198; MUID:77021516
A;Contents: heavy chain disease protein zuc, partial sequence corresponding to residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. Wote: this protein lacks most of the V region, all of the CH1 region, and part of the N. Alexander. A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A.Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deleti A; Reference number: A93915; MUID:82247835
A. Contents: heavy chain disease protein Omm
A. Accession: A93915
A. Molecule type: mRNA
A. Residues: 12-70;72-114;116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-18, Note: a carboxyl-terminal Lys is removed posttranslationally
A. Note: this sequence may represent an allelic form or another gamma chain subclass
C. Commont: The heavy chain disease protein Wis is shown.
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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A;Map position: 14q32.33-14q432.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglut.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
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Pred. No. 2.3e-46;
8; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
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R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A; Reference number: I47158; MUID:95015845
A; Accession: I47162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule, type: mRNÅ
A; Residues: 1-470 < SAN's
A; Residues: 1-470 < SAN's
A; Cross-references: EMBL: X62916; NID:9439; PIDN: CAA44699.1; PID:9440
A; Cross-references: EMBL: X62916; NID:989
Mol. Immunol. 26, 841-850, 1989
A; Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 & A; Reference number: $06610; MUID:90097956
A; Reference number: $06610; MUID:90097956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N.Alternate names: Ig gamma-1 chain C region (clone 8.10)
C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Spate: O6-Jan.1995 #sequence_revision 06-Jan.1995 #text_change 23-Jul-1999
C.Accession: S22080; S06610; A31303
R.Sanders, P.G.
Submitted to the EMBL Data Library, November 1991
A.Reference number: S22080
A.Reference number: S22080
A.Status: preliminary
                                     Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                   A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: the sequence was determined from the germline gene C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.7%; Score 463; DB 2; L
79.8%; Pred. No. 3.2e-39;
iive 13; Mismatches 8;
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Best Local Similarity / ...
best Egg Conservative 1
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A; Residues: 142-470 <SYM>
A; Cross-references: EMBL:X16701
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Best Local Similarity
Matches 83; Conserv
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                                                                                                                             C; Accession: 147162
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                                                                                                                                         147160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
R;Kacskovics, I:; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a R;Reference number: 147150; MUD:95015845
A;Accession: 147160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 147160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C;Genetics: 1-328 ckAC>
A;Gene: IgG2D
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Sus scrofa domestica (domestic ply)

Species: Sus scrofa domestica (domestic ply)

C; Species: Sus scrofa domestica (domestic ply)

C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

R; Accession: 153, 3565-3573, 1994

A; Title: Five putative subclasses of swine 1gG identified from the cDNA sequences of a same ference number: 147159; MUID:95015845

A; Reference number: 147159; MUID:95015845

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Status: preliminary; mannoglobulin C region; immunoglobulin homology

F; 133-202/Domain: immunoglobulin homology < TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
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Length 328;
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80.8%; Pred. No. 1
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Query Match

Best Local

Matches

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Query Match

Best_Local Matches 8

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Search completed: June 21, 2002, 08:37:55 Job time: 429 sec
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C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Accession: 147161
C; Accession: 147161
C; Accession: 147161
A; Title: Five putative subclasses of swine IgG identified from the CDNA sequences of a A; Reference number: 147158; MUID:95015845
A; Accession: 147161
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-328 < KAC>
A; Cross-references: EMBL:U03781; NID:9433127; PIDN:AAA52219.1; PID:9433128
C; Genetics:
A; Gene: IgG3
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 133-202/Domain: immunoglobulin homology < IMM>
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147158
159
169 gamma 1 chain constant region - pig (fragment)
159 species: Sus scrofa domestica (domestic pig)
15. Species: Sus scrofa domestica (domestic pig)
15. Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
15. Accession: 147158
15. Sustler, J.E.
15. Immunol. 153, 3565-3573, 1994
15. Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a striction of the contraction of the con
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Astatus: prelliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 KRAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
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    REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                             Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: IgG1
C,Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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Pred. No. 3.2e-37;
2; Mismatches 10;
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78.6%; Pre
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Best Local Similarity
Matches 81; Conserv
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NAME: Wagner, Richard W.
REGISTRATION UNDBER: 34,480
REFERENCE/DOCKET NUMBER: ALKB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4(CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                             STREET: TWO MAL
                                                                                                                                                                                                                                                                                                                                           CITY:
STATE: MA
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Sequence 2, Appli
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                                                              June 21, 2002, 08:32:16 ; Search time 77.71 Seconds
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-477-460B-2
US-09-329-916-2
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US-09-409-006A-2
PCT-US93-07422-2
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US-08-332-539D-55
US-08-332-539D-55
US-08-936-854-4
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US-09-022-55-4
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US-09-022-259-4
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Sequence 14, A
Sequence 14, A
Sequence 3, A
Sequence 3, A
Sequence 3, A
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Sequence
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Sequence
Sequence
US-09-218-950-33
US-09-178-869-2
US-07-940-861-43
US-08-459-512-43
US-08-460-132-43
US-08-460-132-43
US-09-180-100-11
US-09-180-100-11
US-09-180-100-22
US-09-180-100-22
US-09-131-247-16
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## ALIGNMENTS

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TRANSFERIN RECEPTOR SPECIFIC ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIR Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34,480
ER: ALK88-15AAAZ
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994

PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991

PRIOR APPLICATION NUMBER: PCT/US90/05077

APPLICATION NUMBER: PCT/US90/05077

FILING DATE: 07-SEP-1990

PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989

ATCONEY, AGENT INCPRAFILON:
ANALY: 1900NEY, ANALY: 1900NE
US-08-444-644-30

| Sequence 30, Application US/08444644

| Patent No. 6015555

| GENERAL INFORMATION:

| APPLICANT: Friden, Phillip M.

| TITLE OF INVENTION: TRANSFERRIN RE

| TITLE OF INVENTION: CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,64
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APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIOYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVAGPSVFLFPPKFKDTLMISRIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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Pred. No. 6.2e-57;
4; Mismatches 2; Indels
                                                                                                                       61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/477,460B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-A0G-1992
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                          Sequence 2, Application US/08477460B
Patent No. 6034223
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 42523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.08;
94.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: homo sapien
CELL TYPE: lymphocyte
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                 US-08-477-460B-2
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTHBODY NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCES.
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                              Gaps
                                                                                                                                                                                                 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                          Gaps
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                                                                                                              Score 559; DB 3; Length 109;
Pred. No. 1e-57;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                    61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                           Score 559; DB 4; Length 109;
Pred. No. 1e-57;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY 1994
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: US-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1999
ATPLICATION NUMBER: US-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/08232246A Patent No. 6329508 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                            Query Match
Best Local Similarity 94.5%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.0%;
94.5%;
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Best Local Similarity 94.5
Matches 103; Conservative
                         internal
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// FRAGMENT TYPE: internal
US-08-232-246A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-444-644-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-232-246A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
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1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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Pred. No. 6.2e-57;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS NUMBE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08485372A Patent No. 6187748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                         96.0%;
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                            LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 432 amino acids TYPE: amino acid
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TELEFAX: (212) 391-0525
                                                                                                                                      SS: unknown
unknown
                                                                                                                                                                                                                                                                                                                                                                                     Matches 103; Conservative
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                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapier
                                                                                                                                                                                                                                homo sapien
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CLASSIFICATION: 435
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Best Local Similarity
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: USA
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                                                                                 DEFICANT: Allaway Graham P.

APPLICANT: Allaway Graham P.

APPLICANT: Allaway Graham P.

APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: No. 608478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/O8/379,516
CURRENT FILING DATE: 1996-06-10
EARLIER FILING DATE: 1996-06-10
EARLIER FILING DATE: 1993-08-07
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
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Pred. No. 6.2e-57;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,460
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/329,916 FILING DATE:
US-08-379-516-2
; Sequence 2, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09329916
Patent No. 6177549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: White, John P. REGISTRATION NUMBER: 28,678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.0%;
94.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.5
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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Sequence 2, Application PC/TUS9307422
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                  61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 432;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07422

FILING DATE: 19930806

CLASSIFICATION NUMBER: DCT/US93/07422

FILING DATE: 19930806

CLASSIFICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 07/927,931

FILING DATE: NOT-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9590

TELERX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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Patent No. 6034223
GENERAL INFORMATION:
GAPPLICANT: Progenics Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                           STAREST: COOPER & Dunham STREET: 30 Rockefeller Plaza CITY: New York STAME: New York COUNTRY: USA ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.0%;
94.5%;
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Best Local Similarity 94.5°
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL TYPE: lymphocyte PCT-US93-07422-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                       PCT-US93-07422-2
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APPLICANT: Progenics Pharmaceuticals, Inc.

APPLICANT: Progenics Pharmaceuticals, Inc.

TITLE OF INVENTION: COA-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza
                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                         1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                          0;
                                                                                                                   Length 432
                                                                                                                                                                                                                                                                                                                                       61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                    Score 559; DB 4; Length 432;
Pred. No. 6.2e-57;
4; Mismatches 2; Indels
                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                              Score 559; DB 4;
Pred. No. 6.2e-57;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEX: (212) 977-9809
TELEX: (212) 977-9809
TELEX: (212) 977-9809
TELEX: C2533 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
PRIOR APPLICATION 1 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09409006A
Patent No. 6342586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                              96.0%;
94.5%;
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94.5%;
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                                                                                                                                                                  Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103; Conservative
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     lymphocyte
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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; CELL TYPE:
US-08-485-372A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-409-006A-2
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Gaps

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Sequence 4, Application US/09329916

Patent No. 6177549

GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
ATILE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF NUMBER OF SEQUENCES:
ADDRESSEE: Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                                                                                                                     Score 559; DB 3; Length 530;
Pred. No. 8.1e-57;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.0%; Score 559; DB 4; Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 REEQFINSTERVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 423
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APPLICATION NUMBER: 08/477,460
FILING DATE: 07-40N-1995
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-80G-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                        96.0%;
94.5%;
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TELEFAX: (212) 977-9809
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 4:
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                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 530
                                                                                                                                                                                                                                                                     Query Match 96.0
Best Local Similarity 94.5
Matches 103; Conservative
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unknown
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CELL TYPE: lymphocyte
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                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 30 Rocker
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CORIGINAL SOURCE:
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US-09-329-916-4
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Sequence 4, Application US/08379516

Sequence 4, Application US/08379516

Sequence 4, Application US/08379516

Sequence 4, Application US/08379516

GENERAL INFORMATION:

APPLICANT: Allaway, Graham P.

APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: No. 608478-Peptidyl Moiety-Conjugated CD4-Camma2 and CD4-IgG2

TITLE OF INVENTION: Immunoconjugates and Uses Thereof

FILE REFERENCE: 41215-A-PCT-US

CURRENT APPLICATION NUMBER: US/08/379,516

CURRENT FILING DATE: 1996-06-10

EARLIER APPLICATION NUMBER: PCT/US93/07422

EARLIER PILING DATE: 1993-08-06

EARLIER FILING DATE: 1992-08-07

NUMBER OF SEQ ID NOS: 9
                         NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 559; DB 3; Length 530;
Pred. No. 8.1e-57;
4; Mismatches 2; Indels
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SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/47,460B

FILING DATE: 07-JUN-1995

CLASSIFICATION 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P. REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 10FORMATION:

TELECOMMUNICATION 2017

TELECOMMUNI
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 96.0%;
Best Local Similarity 94.5%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CELL TYPE: lymphocyte US-08-477-460B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 559; DB 4; Le
Pred. No. 8.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41215-A-PCT/JPW/AJM
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GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                              Sequence 4, Application US/09409006A
Patent No. 6342586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEX: (212) 977-9809
TELEX: 4.2553 COP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                  ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
                                                                                                                                                                            TITLE OF INVENTES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COOPER & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.0%;
Best Local Similarity 94.5%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE: lymphocyte US-09-409-006A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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MOLECULE TYPE: c
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                          COUNTRY: US
                                                              US-09-409-006A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US93-07422-4
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                                                                                              Gaps
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                                                                          1 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 530;
                                                                                                                                                    61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                          61 BEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
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                                                                                                                                                                                                                                                                              Sequence 4, Application US/08485372A
Patent No. 6187748
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
Pred. No. 8.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 559; DB 4;
Pred. No. 8.1e-57;
                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATOMNE: White, John P.
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 37690-II-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                    94.5%;
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Best Local Similarity 94.5%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                      Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE: lymphocyte US-08-485-372A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
: New York
                  Best Local Similarity
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COUNTRY:
                                                                                                                                                                                                                                                              US-08-485-372A-4
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TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF

CORRESPONDENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham
  ö
                                                                                    315 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 374
     Gaps
                                                  1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
  ö
                                                                                                                                                                                       61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
Indels
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56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
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Pred. No. 1.5e-57;
1; Mismatches 1; Indels
                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION NUMBER: 07/744768
FILING DATE: 14-40G-1991
ATTORNEY/AGBNT INFORMATION:
NAME: SYODOGA, Craig G.
REGISTRATION NUMBER: 90/18P3
TELEPHONE: 650/225-1489
TELEPAX: 650/225-1489
TELEPAX: 650/225-1489
TELEPAX: 650/225-1489
TELEPAX: 100 NO: 55: 550/100 NO: 55: 55
          APPLICATION NUMBER: US/08/232,539D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 21, 2002, 08:32:16 Job time: 90 sec
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93.0%;
                                           21-Apr-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.9
Best Local Similarity 93.0
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , TOPOLOGY: Linear
US-08-232-539D-55
                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 559; DB 5; Length 530;
Pred. No. 8.1e-57;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                             PRICE DATE: 19930806
CLASSIFICATION:
PRICE APPLICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-80G-1992
ATORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERA: (212) 977-9550
TELERA: (212) 977-9560
TELERA: (212) 977-9560
TELERA: (212) 977-9560
TELERE: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANBONESS: unknown
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windatin (Geneticch)
CURRENT APPLICATION DATA:
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Sequence 55, Application US/08232539D
Patent No. 5965709;
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IGE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
                                                                                                                                                                              COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Pair
      30 Rockefeller Plaza
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 96.0%;
Best Local Similarity 94.5%;
Matches 103; Conservative
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                                                                                                                               ZIP: 10112
COMPUTER READABLE FORM:
                                        New York
New York
                                                                                                       USA
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STREET:
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CD4-gamma2 chimeri Humanised 323/A3 ( Human IgG2 chain C The heavy chain of Humanised 323/A3 (

Human CD4-gamma2

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ALIGNMENTS
                                                                   AAB26884
AAY93701
AAY93707
                                                                                            AAY93727
AAY93732
AAY93703
AAY93730
                                                                                                                                       ARE26783

AARB6080

AAB67323

AAY42621

AAR87262

AAR97263

AAW62305

AAW47354

AAW92411

AAY99977

AAY97250

AAR97250
        AAY85079
AAB80883
                                  AAB72230
                                                                                                                                AAW38415
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                                                                                                                                                                                                                                                                                                                                                               AAY54996 standard; protein; 109
17-FEB-2000 (first entry)
AAY54996;
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RESULT
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2: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1980.DAT:*
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11: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1982.DAT:*
12: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1982.DAT:*
13: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1982.DAT:*
14: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1992.DAT:*
15: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1992.DAT:*
16: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1992.DAT:*
18: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1992.DAT:*
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20: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1992.DAT:*
21: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1992.DAT:*
22: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\AA1992.DAT:*
                                                         ; Search time 224.82 Seconds
(without alignments)
53.852 Million cell updates/sec
                                                                                                              1 APPVAGPSVFLFPPKPKDTL......CKVSNKALPAPIEKTISKAK 109
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                         747574 seqs, 111073796 residues
                                                                                                                                                                                                                                      Listing first 45 summaries
                                            protein search, using sw model
                                                           June 21, 2002, 08:36:09
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Maximum DB seq length: 2000000000
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                                                                                            US-09-674-857-9
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**BLOSUM62** 

Scoring table:

Searched:

Perfect score:

Title:

Sequence:

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OM protein

Run on:

Maximum

Database

Human immunoglobul
The heavy chain of
CD4 -19G2 chimeric
CD4 -19G2 chimeric
CD4 -19G2 chimeric
Human CD4 -1GG2 chi
CD5 -1GG2 chi
CD5 -1GG2 chi
CD6 -1GG2 chi
CD7 -1GG2 chi
CD6 -1GG2 chi
CD7 -1GG2 c

Human 19G1 Fc regi Human immunoglobul 19G1 Fc protein us

Human immunoglobul

regi

Human 1961 Fc Human 1961 Fc

Human immunoglobul Human immunoglobul

Fc region of human Fc region of human Human immunoglobul

Sequence of human

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Mutated CH2 sequen	Rat Thy-1-human Ig	Human Thy-1-human	Humanised anti-CD2	Undefined ORF2 enc	Amino acid sequenc	Human IgG2. Homo	Human IgG2 Fc regi	Human immunoglobul	Human IL-2/Ig fusi	CD4-gamma2 chimeri
qi	AAY54996	AAY31788	AAY31789	AAY32263	AAR41709	AAB07476	AAB67203	AAB76423	AAE02643	AAY06895	AAR26782
DB :	21	20	20	21	14	21	22	22	22	20	13
Query Match Length DB ID	109	368	368	444	109	217	217	217	326	381	432
Query Match	97.4	96.3	96.3	96.3	96.0	96.0	96.0	96.0	0.96	0.96	96.0
Score	267	560.5	560.5	560.5	559	559	559	559	559	559	559
Result No.	1	7	æ	4	S	9	7	80	თ	10	11

cell.mediated destruction; human; immunoglobulin G; 1gG heavy chain; cell.mediated destruction; human; immunoglobulin G; 1gG heavy chain; crohn's disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune disorder; autoimmune hamolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; crythroblastosis foetalis; enconatal alloimmune thrombocytopaenia; cooparatic sorgan transplant sickle cell anaemia; coronary artery occlusion. Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD Ë Clark MR, Williamson Mutated CH2 sequence Gldeltaab. 99WO-GB01441 98GB-0009951 07-MAY-1999; WO9958572-A1 08-MAY-1998; 18-NOV-1999. ĸĽ, Synthetic. Armour  99WO-US05256.

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(HARD ) HARVARD COLLEGE (HABE/) HABER C.
        W09945951-A2
                                                                                      11-MAR-1999;
                                                                                                                              11-MAR-1998;
                                                  16-SEP-1999.
          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                   This sequence represents the mutated CH2 molecule Gldeltaab, and is a binding molecule of the invention. The recombinant binding molecule of binding a target molecule without tringering complement dependent lysis, or the cell-mediated destruction of the target molecule. Comprises: (a) a binding domain capable of binding a target molecule; and domain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FogammaRIIb molecule is used to bind a target molecule (especially FogammaRIIb phagocytosis). The binding molecule can be used to prevent or inhibit the binding of a second binding molecule, e.g. an antibody, to the target molecule. The binding molecule is useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                      graft-vs-host disease, organ transplant rejection, bone-marrow transplant autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia, autoimmune thrombocytopeania and arthritis), alloimmunity anaemia, autoimmune thrombocytopeania and arthritis), alloimmunity cergetal/neonatal alloimmune thrombocytopeania, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through Fogamma and desirable 1gG properties have been retained. The polypeptides do not contain immunogenicity. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FCRN (neonatal FC receptor).
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                                   Immunoglobulin-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.306 -...
/label= "mature Thyr-11g, specifically claimed in
Claim 8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thy-1; rat; human; IgG; angiogenesis; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Thy-1-human IgG constant region fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 567; DB 21;
Pred. No. 2.4e-49;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; atherosclerosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Thy-1 signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.46
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY31788 standard; Protein; 368 AA.
                                                                                                               Claim 12; Fig 17; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.4%;
97.2%;
                                                                             immunoglobulin properties -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.2
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Rattus sp.
Chimeric - Homo sapiens.
WPI; 2000-039075/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY31788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY31788
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The present sequence represents a fusion protein, the mature portion of which is claimed, comprising the rat Thy-1 extracellular region (see also ARY31786) and the constant region (hinge, CH2, CH3) of human IgG1. The fusion protein was transiently expressed in COS cells transfected with an expression plasmid containing a chimeric DNA (see ARX8999). A claimed method for inhibiting angiogenesis in a mammal comprises administering a compound that inhibits Thy-1 associated proliferation of an endothelial cell. This compound is preferably the extracellular region of rat or human Thy-1. The method is used in the treatment of a mammal having a tumour (e.g. by reducing vascularisation), atherosclerosis or rheumatoid arthritis, the lesions of which may be associated with neovascularisation (all claimed). Another claimed method for inhibiting angiogenesis involves administering a Thy-1 antisense nucleic acid or a Thy1-specific antibody linked to a cytocoxic agent. A method for promoting angiogenesis involves administering a compound that increases Thy-1 expression in an endothelial cell fragment and the constant region of an immunoglobulin.
                                                                                                                  Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APPVA----GPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Thy-1-human IgG constant region fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thy-1; human; 19G; angiogenesis; cancer; tumour; rheumatoid arthritis; atherosclerosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 560.5; DB 2
Pred. No. 4.6e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
     Lee W;
                                                                                                                                                                                        Claim 8; Page 45-46; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY31789 standard; Protein; 368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ξ;
     Jain MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.3%;
93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Homo sapiens.
                                            WPI; 1999-561618/47.
N-PSDB; AAX87979.
Shaw S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 AA;
                                                                                                                                                 angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1999
Haber E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY31789;
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1;

3

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Sequence
 1;
                                                                                                                                                                                                                                                                              The present sequence represents a fusion protein, the mature region of which is claimed, comprising the human Thyl extracellular region (see AAY31787) and the constant region (hinge, CH2, CH3) of human 1gGl. A claimed method for inhibiting anglogenesis in a mammal comprises administering a compound that inhibits Thyl associated proliferation of an endothelial cell. The compound is preferably the extracellular region of rat or human Thyl. The method is used in the treatment of a mammal having a tumour (e.g. by reducing vascularisation), atthereosclerosis or rheumatoid arthritis, the lesions of which may be associated with neovascularisation (all claimed). Another claimed method for inhibiting anglogenesis involves administering a Thyl.
                                                                                                                                                                                                                               Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVA-----GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                              antisense nucleic acid or a Thyl specific antibody linked to a cytotoxic agent. A method for promoting angiogenesis involves administering a compound that increases Thyl expression in an endothelial cell such as a chimeric protein comprising the Thyl extracellular fragment and the constant region of an immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.368
18.368 "Thy-1-Ig fusion, specifically claimed Claim 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20; Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5; ...
4.6e-48;
         /note= "Thy-1 signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.3%; Score 560.5;
93.9%; Pred. No. 4.6e
ative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised anti-CD23 MAb C11 heavy chain.
                                                                                                                                                                              Lee W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY32263 standard; Protein; 444 AA
                                                                                                                                                                                                                                                            Claim 8; Page 46-47; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     llarity 93.9%;
Conservative
                                                                                                     99WO-US05256.
                                                                                                                          98US-0077524
                                                                                                                                                                             Shaw S, Jain MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                              (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                WPI; 1999-561618/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 AA;
                                                                                                                                                                                                           N-PSDB; AAX87980
                                                                                                                                                        HABE/) HABER C.
                                                                                                                                                                                                                                          anglogenesis
                                                            W09945951-A2
                                                                                                     11-MAR-1999;
                                                                                                                          11-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2000
                                                                                  16-SEP-1999
                                                                                                                                                                             Haber E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Peptiale
                    Protein
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This amino acid sequence represents the heavy chain of humanised anti-CD23 (FCERII) monoclonal antibody Cl1, composed of a human canti-CD23 (FCERII) and the heavy chain complementarity determining regions (see AAY32257-59) of murine antibody Cl1. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprises sufficient of the amino acid sequences of the Cl1 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on meamatopoidatic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, labetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, colitis, Crohn's disease, COPD, insulitis, bronchitis ecema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell receptor specific antibodies useful for treating e.g. arthritis.
inflammation, arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shearin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rapson NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104..111
/note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetes, multiple sclerosis and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112..444
/note= "constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ellis JH,
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.100
/note= "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determining the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "CDR 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CDR 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CDR 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 4; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-GB01434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98GB-0009839.
                                                                                                                                                                                                 B-cell malignancy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonnefoy JMP, Crowe SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    31..35
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
50..68
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N-PSDB; AAZ34748.
                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09958679-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-1999.
                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                               Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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444 AA;

us-09-674-857-9.rag

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Length 109;

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The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma—2, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a muran source and the sequences encoding CHI, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ4845), was transfected into SP2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to encropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, and Albs, stroke, epilepsy, Parkinsons and Alzheimers disease. It may
                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transfertin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                              Gaps
                                                                          1 APPVAG-PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
                                   1;
 Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                         288 preegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskak 337
                                                                                                                                                   60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                       1; Indels
DB 21;
                   .8e-48;
Score 560.5;
Pred. No. 5.8e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Undefined ORF2 encoded by plasmid pAH4625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 17J; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stroke, epilepsy, Parkinsons a
be used for diagnostic methods.
                                                                                                                                                                                                                                                                                   AAR41709 standard; Protein; 109 AA.
Query Match 96.3%;
Best Local Similarity 97.3%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-US10206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-0800458
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ALKE-) ALKERMES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-196742/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ43846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                            20-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9310819-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Friden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders
                                                                                                                                                                                                                                                                                                                         AAR41709;
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AAB07474-78 represent native IgG Fc regions. The proteins are used to produce Fc region-containing polypeptides that have altered effector function as a consequence of one or more amino acid modifications in the Fc region. The variant polypeptides are useful for treating cancer, allergic conditions such as asthma (with an anti-lgE antibody), and LFA-1-mediated disorders. Where the polypeptide binds the HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a benign or malignant tumnour characterized by overexpression of the HER2 receptor. Such cancers include breast cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer, colorectal cancer, inver cancer, liver cancer, liver cancer, liver cancer, liver cancer, liver cancer, liver cancer, hepatoma, types of head and neck cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Fc region-containing polypeptides that have altered effector function due to one or more amino acid modifications in the Fc region, useful in the treatment of cancer and allergic conditions such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                   Gaps
                                                                  1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                    1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                         IgG antibody; light chain; Fc region; effector function; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 559; DB 21; Length 217;
Pred. No. 3.5e-48;
                                                                                                                                    REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                         allergy; asthma; LFA-1-mediated disorder; tumour; cancer
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                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of native IgG Fc region humIgG2.
Score 559; DB 14;
Pred. No. 1.5e-48;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
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                                                                                                                                                                                                                                                        AAB07476 standard; protein; 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.08;
94.58;
96.0%;
ilarity 94.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2000; 2000WO-US00973.
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                                                                                                                                                                                                                                                                                                                         20-OCT-2000 (first entry)
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Best Local Similarity
Matches 103; Conserv
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-1999;
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 Query Match
Best Local Simi
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Presta LG;
                                                                                                                                                                                                                                                                                      AAB07476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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AAB67203

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This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides cepresented in AAB7630 - AAB76420 and AAB76432 - AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences used in the invention. Sequences used in the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, disorders of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, atrokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat alzease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease
                                                                           Human, erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Menlere's disease; diabetic neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 appvagpsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwyvdgvevhnaktkp 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunoglobulin G2 constant region mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 559; DB 22;
Pred. No. 3.5e-48;
4; Mismatches 2;
                                           Human IgG2 Fc region amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Figure 2A; 116pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match . 96.0%;
Local Similarity 94.5%;
les 103; Conservative 4
                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000WO-US18283
                                                                                                                                                                                                                                                                                                                            99US-0142232
   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 AA;
                                                                                                                                                                                                             WO200101748-A2
                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2001
   10-APR-2001
                                                                                                                                                                                                                                                   11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                       Dennis MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 appvagpsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwyvdgvevhnaktkp 61
The present invention relates to a fusion protein, comprising a peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (Ib). The hybrid molecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used example the peptide ligand can bind ErbB2. The peptide ligand may bind to and inhibit the activity associated with a particular
                                                                                                                                                                                                                                                                                                                                              Fusion protein; immunoglobulin; multidimerization domain; ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                       Indels
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Pred. No. 3.5e-48;
4; Mismatches 2;
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                                                                                                                                                                                        AAB67203 standard; protein; 217
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                                                                                                                                                                                                                                                                       entry)
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Best Local Similarity 94.5
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lazarus RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                     (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        target molecule
                                                                                                                                                                                                                                                                                                                                                                                                                       WO200102440-A1
                                                                                                                                                                                                                                                                                                                                                                                    Homo saptens.
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                                                                                                                                                                                                                                                                     10-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dennis MS,
                                                                                                                                                                                                                                                                                                          Human IgG2.
                                                                                                                                                                                                                               AAB67203;
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AAB76423

Homo sapiens,

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The present sequence is human immunoglobulin G2 (1gG2) constant region mature protein. IgG2 forms a fusion protein with human erythropoietin (EPO). EPO has improved biological activity and an extended serum half life greater than 20 hours. The present invention relates to modified composition broteins comprising a FC portion of an immonglobulin (Ig) molecule and an EPO molecule (FC-EPO). The FC portion is fused covalently through its C-terminus directly or indirectly to the EPO molecule, and where the FC portion as well as EPO portion may be modified or mutated. The invention also relates to non-fused EPO molecules which have a pattern of cysteines or disulphide bonding which is distinct from human or animal EPO. Pharmaceutical compositions containing EPO are useful in the treatment of EPO deficient diseases such as anaemia, renal failure, HIV infection, blood loss and chronic disease.
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                                                                                                                                                                                                                                                                                                                                                         Novel modified erythropoietin forms such as fusion proteins, comprising FC portion of an immunoglobulin molecule and a target molecule having the biological activity of erythropoietin forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein; vaccine; cytokine; immunoglobulin; autoimmune disease; inféctious disease; inflammatory disease; neoplastic disease; cancer; immunologic disease; immune response; malaria; tuberculosis; hepatitis; AIDS; influenza; interleukin; IL-2; Ig; human.
Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV; vacchae; haemostatic; immunoglobulin G2; IgG2; EPO deficient disease; anaemia; renal fallure; Human Immunodeficiency Virus; HIV; haematopoietic growth factor.
                                                                                                                                                                                                                                                                                                 Gillies S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                                                                                                                                                 Way JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
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                                                                                                                                                                                                                                                                                             Sobel C,
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                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 24; 58pp; English.
                                                                                                                                                                                                                                                                                            Rieke E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IL-2/Ig fusion protein.
                                                                                                                                                                                       03-NOV-2000; 2000WO-EP10843
                                                                                                                                                                                                                                                        (MERE ) MERCK PATENT GMBH.
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                                                                                                                                                                                                                                                                                          Brandt S,
                                                                                                                                                                                                                                                                                                                          WPI; 2001-367563/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                 WO200136489-A2.
                                                                                  Homo sapiens.
                                                                                                                                                                                                                       12-NOV-1999;
                                                                                                                                                     25-MAY-2001.
                                                                                                                                                                                                                                                                                          Hartmann A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1999
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Best Local Si
Matches 103,
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The invention relates to vaccine compositions comprising a vaccine and a timed-release formulation of a cytokine or cytokine/immunoglobulin fusion timed-release formulation of acytokine releases the cytokine protein or plasmid at one or more temporal points subsequent to vaccine protein or plasmid at one or more temporal points subsequent to vaccine administration. The vaccines can be used for treating an autoimmune disease, an infectious disease, an inflammatory disease, a neoplastic disease, or an immunologic disease in an individual. The vaccines can be used to elicit immune responses against diseases such as AIDS, malaria, tuberculosis, hepatitis C, hepatitis B, cancer or influenza. The methods can provide for enhancement of one or more immunologic parameters such as an antibody response, a cellular proliferative response as well as cytotoxic T-lymphocyte levels. In addition the Ig can increase the circulating half life of the cytokine. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery; chimeric; increased serum half life; HIV infection; AIDS; ss.
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Pred. No. 6.8e-48;
4; Mismatches 2
                                                     //note= "interleukin-2 (IL-2)"
                                                                                                                                                                                                                                                          (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                        /note= "immunoglobulin G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD4-gamma2 chimeric heavy chain homodimer.
                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Fig 10A-E; 66pp; English.
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Best Local Similarity 94.5%;
Matches 103; Conservative
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                                                                                                                                                                                98WO-US20321
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                                                                         154..381
                                                                                                                                                                                                                                                                                                                                                                     New vaccine compositions
                                                                                                                                                                                                                                                                                           Letvin NL;
                                                                                                                                                                                                                                                                                                                      WPI; 1999-254931/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 AA;
                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX34598
                                                                                                                   W09916466-A2
                                                                                                                                                                                29-SEP-1998;
                                                                                                                                                                                                                          29-SEP-1997;
                                                                                                                                                                                                               L2-DEC-1997;
                                                                                                                                                                                                                                                                                         Sarouch DH,
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                                           Protein
                                                                         Protein
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                              Key
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Homo sapiens chimeric.

W09213947-A 20-AUG-1992

Domain Domain Domain

Key

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CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected subjects to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate comprising the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CD4-gamma 2 chimeric heavy chain homodimer amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to image
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 432;
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Pred. No. 7.9e-48;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 3; 142pp; English.
                                                                                                                Hinge Region.
                                                                                                                                  /label= CH2 Region.
326..432
                                      Location/Qualifiers
                                                          1..204
/label= CD4 Region.
                                                                                                                                                                    326..432
/label= CH3 Region.
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94.5%;
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                                                                                          205..216
/label= Hi
217..325
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Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and stage HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                       Allaway GP, Maddon PJ;
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  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a CD4-gamma2 chimeric heavy chain homodimer. It was produced by expression of the coding mutagenised CDNA (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV of. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, eg biphtheria, pseudomonas exotoxin A (domainS I or II) or the deglycosylated A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV; human immunodeficiency virus; radionuclide; toxin; therapy; treatment; imaging; detection; targetting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt CD4-gamma-2} and {\tt CD4-IgG2} chimera(s) and expression vectors - for treatment, prevention and diagnosis of HIV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 3; 90pp; English.
                                      /label= CD4
217. 336
                                                                      217..325
/label= CH2
326..433
/label= CH3
                                                                                                                                                                                                                                                92WO-US01143
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                                                                                                                                                                                                                                                                                                                                                               Beaudry GA, Maddon PJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 AA;
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Sequence

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AAR46678;

RESULT 12 AAR46678

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Gaps

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AAB80883 standard; Protein; 432 AA.

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This sequence represents the human CD4-gamma 2 chimeric heavy chain chandimer amino acid sequence. The invention relates to an chandimer amino acid sequence. The invention relates to an invention by the composition of the control than an expectation of two heavy chains and two light chains. The cytotoxic radionuclide is linked to either the heavy chains or the light chains, or to all four chains, directly or through a bifunctional chelator. Both heavy chains of chains, directly or through a bifunctional chelator. Both heavy chains of chains, directly or through a bifunctional chelator. Both heavy chains of chains are chimeric CD4-180 (amunoglobulin) G2 chains encoded by vector CD4-180 (and poth light chains are chimeric CD4-180 (and poth light chains are chimeric CD4-180 can both light chains are chimeric CD4-180 can light calls of the monocyte/macrophage lineage of non-polymorphic cells us face of lyopprotein that is expressed on the surface of helper T lymphocytes, cells of the monocyte/macrophage lineage and dendritic cells. CD4 associates with major histocompatibility complex (MHC) class II molecules on the surface of antigen presenting cells to mediate efficient cellular immuno response interactions. In humans CD4 is the target of interaction with the human immunodeficiency virus HTV. The manoconjugate is used to kill cells infected with HTV, and for treatments). The immunoconjugate is also used for imaging HTV-infected tissues (for staging and prognosis of HTV infected patients. The immunoconjugate should be active against all strains of HTV (since the immunoconjugate should be active against all strains of HTV (since the immunoconjugate should be active against all strains of HTV (since the immunoconjugate should be active against all strains of CD4-9p120 interaction is essential for infection). The heterotetraners collinears and purification from the culture medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to heterotetramer of CD4-immunoglobulin chimeras
    staging; prognosis; envelope glycoprotein burden; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3; 58pp; English.
                                                                                                                                                                                        95US-0477460.
                                                                                                                                                                                                                                      92US-0927931.
                                                                                                                                                                                                                                                                                    95US-0379516.
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                                                                                                                                                                                                                                                              93WO-US07422
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                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ98855
                                                  Homo sapiens.
                                                                                                                                                                                     07-JUN-1995;
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03-FEB-1995;
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432 AA; Sequence

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                                                                1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
Score 559; DB 21; Length 432;
Pred. No. 7.9e-48;
4; Mismatches 2; Indels
                                                                                                    REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
 96.0%;
94.5%;
                       Matches 103; Conservative
             Similarity
Query Match
             Best Local
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RESULT 14 AAB80883

277

(first entry)

23-APR-2001

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The present invention relates to a method for inhibiting infection of a cold+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimeric heterotersmer to form a complex with the HIV (CD4 = cluster of differentiation 4: IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of reals. In and, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors tas used to inhibit infection of a CD4+Ccll by a HIV and to prevent CD4+cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4+cells infected with HIV. The present sequence is human fusion protein: CD4-gamma2 chimeric heavy chain homodimer. This sequence was used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell, or treating a subject having CD4+ cells infected with HIV involves using CD4-IgG2 chimeric heterotetramer to form a complex with the HIV -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Anti-HIV; CD4-1gG2 chimeric heterotetramer;
                                                                                            Human CD4-gamma2 chimeric heavy chain homodimer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3; 55pp; English.
                                                                                                                                                                                                                                                                                                 91US-0653684.
92WO-US01143.
92US-0960440.
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                                                                                                                                                                                                                                                                                                                                                              (PROG-) PROGENICS PHARM INC
                                                           29-MAY-2001 (first entry)
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Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Beaudry GA;
                                                                                                                                            immunoglobulin gamma 2.
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N-PSDB; AAF77829.
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                                                                                                                                                                          Homo sapiens.
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08-DEC-1992;
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                             AAB80883;
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Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappaalight chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterotetramer having two chimeric CD4-1gG2 heavy chains encoded by an expression vector CD4-1gG2HC-PRCCWV and two chimeric CD4-kappa light chains encoded by an expression vector CCG4-LC-PRCKW. The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, for the treatment and prevention of infection with HIV.
            CD4-gamma2 chimeric heavy chain homodimer protien.
                                         Immunoconjugate; chelator; chimeric; HIV;
human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 3; 43pp; English.
                                                                                                                                                                                                   95US-0477460.
92US-0927931.
93US-0379516.
93WO-US07422.
                                                                                                                                                                         99US-0329916.
                                                                                                                                                                                                                                                                             (PROG-) PROGENICS PHARM INC
                                                                                                                                                                                                                                                                                                          Maddon PJ, Allaway GP;
                                                                                                                                                                                                                                                                                                                                    WPI; 2001-158582/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 AA;
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07-AUG-1992;
06-AUG-1993;
06-AUG-1993;
                                                                                                               US6177549-B1.
                                                                                     Homo sapiens
                                                                                                                                                                        10-JUN-1999;
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Gaps

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Search completed: June 21, 2002, 08:36:09 Job time: 323 sec

1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

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Query Match 96.0%; Score 559; DB 22; Length 432; Best Local Similarity 94.5%; Pred. No. 7.9e-48; Matches 103; Conservative 4; Mismatches 2; Indels (

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sapien

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Perfect score:

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Scoring table:

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Minimum DB Maximum DB

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Hu Z., Garen A.;
"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
EMBL, AF272774; AAK58686.1, ...
SEQUENCE 701 AA, 77826 MW; 94AC6CEB42CC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PP-----VAGPSVFLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 95.9%; Score 558; DB 4; Length 701; Best Local Similarity 93.0%; Pred. No. 6e-53; Matches 106; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
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Q95m34 equus cabal
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                                                                                                                                                                                             1 APPVAGPSVFLFPPKPKDTL......CKVSNKALPAPIEKTISKAK 109
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                              Compugen Ltd
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                          OM protein - protein search, using sw model
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EMBL; AJ300675; CAC44624.1; -.
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                                                                                                                                                                                                                                                                                                             4 VAGPSVFLFPPKPFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
                                                                           Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                         78.0%; Score 454; DB 6; Length 337; 75.5%; Pred. No. 7e-42; tive 16; Mismatches 10; Indels
                                                                                                                                     Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                   QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5C3A7BB3EE7D697C CRC64;
        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        437
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01-MAY-2000 (TIEMBLRE1. 13, Last seque:
01-DEC-2001 (TIEMBLRE1. 19, Last annots
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00290; IG_MHC; UNKNOWN_1
                                                                                                                                                                   MEDLINE=98383416; PubMed=9717671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48142 MW;
                                                                                                                                                                                                                                                                                  Local Similarity 75.59 tes 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                 Equus caballus (Horse).
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                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                 NCBI_TaxID=9796;
                                                (FRAGMENT).
                                                                                                                             Wagner B.;
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SEQUENCE
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Matches
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                                                                         SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 67
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1810060009RIR PROTEIN.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBL_TaxID=10090;
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       Length 437;
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                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC000435; AAH03435.1; -- HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG_MHC; UNKNOWN_1.
51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                   68 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 411; DB 11;
Pred. No. 5.2e-37;
18; Mismatches 12;
                                                                                                                                                                                                                                                                                               463 AA
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                                                                                                                                                                                                                                                                                           PRT;
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InterPro; IPR003599; IG.
InterPro; IPR003509; Ig.cl.
InterPro; IPR003500; Ig_like.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR0040; IG. 2
SMART; SM00409; IG. 2
SMART; SM00407; IG. 2
SMART; SM00410; IG. 12
SMART; SM00410; IG. 12
SMART; SM00410; IG. 12
INTERPROSITE; PS00290; IG_MHC; UNKNO SEQUENCE 463 AA; 51007 MW;
70.68;
70.68;
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                 Best Local Similarity 70.69
Matches 72; Conservative
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Best Local Similarity 70.6%
Matches 72; Conservative
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Fri Jun 21 09:21:24 2002

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STRAIN-C57BL/63; TISSUE-PANCREAS;

KARIN-C57BL/64; TISSUE-PANCREAS;

KARIN-C57BL/64; TISSUE-PANCREAS;

KARIN-C57BL/64; TISSUE-PANCREAS;

KARAWA T., BINGAGWA A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rochim P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quadkenbush J.,

Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Bara J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchioni L., Mashima J., Mazsarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Hayashizaki Y.,

Wayshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Nature A., No. Ase E., Rocholon, A., Nature CDNA collection.";

"Teructional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PPVA-----GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.2%; Score 391; DB 11; Length 473; 63.2%; Pred. No. 9.2e-35; ive 18; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; AAH10327.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA PROTEIN.
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MIC.
InterPro; IPR003596; Ig_MIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1;
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00047; 19; 4.
SMART; SW00409; 1G; 2.
SMART; SW00409; 1Gc1; 3.
SMART; SW00406; 1Gc1; 3.
SWART; SW004106; 1Gv1; 3.
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Matches 72; Conserv
SEQUENCE FROM N.A.
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NCBI_TaxID=10090;
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                                                                                                                                                   263 GPSVFIFPPNIKDVLMISLIPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                              Gaps
                                                                                                                   6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; MusinCBI_TaxID=10090;
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Length 473;
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                                                              18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG_MHC; UNKNOWN_1.
51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                66 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                          323 NSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.8%; Score 383; DB 11;
66.0%; Pred. No. 6.9e-34;
iive 17; Mismatches 19;
     DB 11;
  Score 386; DB 11;
Pred. No. 3.3e-34;
                       66.3%; Pred No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILAR TO RIKEN CDNA 1810060009 GENE
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003599; Ig.
Interpro; IPR003597; Ig.C1.
Interpro; IPR003600; Ig_Ilike.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-DEC-2001 (TrEMBLrel, 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.03
Matches 70; Conservative
                                                              69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , 19; 4.
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SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                   Best Local Similarity
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SEQUENCE FROM N.A.
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     Query Match
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                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      Ö9BSZ1;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYOTHERICAL 41.3 KDA PROTEIN.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                        65.8%; Score 383; DB 11; Length 473; 66.0%; Pred. No. 7e-34; 1ive 17; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-LYMPH, LYMPHOMA;

TISSUE-LYMPH, LYMPHOMA;

Strausberg R.;

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC004476; AAH04476.1; -.

R HSSP; P01857; 1FC1.

R InterPro; IPR003597; 1g_c1.

R InterPro; IPR003606; 1g_like.

R InterPro; IPR003060; 1g_like.

R Pfam; PF00047; 1g; 3.

R SMART; SM00410; 1G_like; 1.

R SMART; SM00410; 1G_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.4%; Score 142; DB 4; Length 375; 28.7%; Pred. No. 1.8e-07; Live 26; Mismatches 44; Indels
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                               Pfam; PF00047; 19; 4.
SMART; SM00409; 1G; 2.
SMART; SM00400; 1Gcl; 3.
SMART; SM00400; 1Gcl; 3.
SMART; SM00410; 1G_like; 1.
PROSITE; PS00290; 1G_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
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375 AA; 41314 MW; BIAOA0998F473619 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                375 AA.
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                   HSSP; P01842; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_MC.
                                                                                                                                                                                                                                70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                     Local Similarity
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Hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                           Query Match
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Matches
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Q9BSZ1
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|| || :: :::: ::||:| |:: | |:| | 368 VFAIPPS-FASIFLIKSTKLTCLVTDLTIYD-SVIISWIRQNGEAVKIHINISESHPNAT 425
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                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006180; AAH06180.1; -.
R EMBL; BC001872; AAH01872.1; -.
R HSSP; POLBZ5; JFAB.
R InterPro; IPR003599; Ig.:
InterPro; IPR003599; Ig.:
InterPro; IPR00350; Ig_AHC.
R InterPro; IPR003506; Ig_AHC.
R InterPro; IPR003506; Ig_AHC.
R R SWART; SW00407; IG; 2.
SWART; SW00407; IG; 2.
R SWART; SW00406; IG.; 1.
R SWART; SW00406; IG.; 1.
R SWART; SW00410; IG.]; 4.
R SWART; SW00410; IG.]; 4.
R SWART; SW00410; IG.]; 6.
R SWART; SW00410; IG.]; 6.
R SWART; SW00410; IG.]; 7.
R SWART; SW00410; IG
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SEQUENCE FROM N.A.
TISSUB-LYMPH, LYMPHOMA;
Strausberg R.;
Interpro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                     01-JUN-2001 (TrEMBLE). 17, Created)
01-JUN-2001 (TrEMBLE). 17, Last sequence update)
01-DEC-2001 (TrEMBLE). 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
597 AA.
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=RHABDOMYOSARCOMA;
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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NCBI_TaxID=9606;
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Q96GA6
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Q96AA6
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                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                           Length 597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. E015760; AAH15760.1; -. Hypothetical protein. SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                                      l protein.
597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
HOMO Saplens (Human).
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:20337).
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                                       InterPro; IPR003596; Ig_v.
Pfan; PF00047; 19; 5.
SMART; SM00407; IGc1; 4.
SMART; SM00406; IGc1; 4.
SMART; SM00410; IGc1; 4.
SMART; SM00410; IG_LIKe; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
HYPOCHECICAL Protein.
SEQUENCE 597 AA; 65274 MW; 2DAFA8F!
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
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Matches 29; Conservative
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SEQUENCE FROM N.A.
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Q96EY0
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo
                                                     Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOLBS7; AAH11857.1; -
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009851; AAH09851.1; -
SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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HYPOTHETICAL 67.8 KDA PROTEIN.
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SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
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TISSUE=LYMPH, AND LYMPHOMA;
Strausberg R.;
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Matches 29; Conservative
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RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

BR MEMEL; BC017356, AM17356.1; -.

KW HYPOThetical protein.

SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match

Best Local Similarity 28.7%; Pred. No. 3.4e-07;

Matches 29; Conservative 26; Mismatches 44; Indels 2; Gaps 2;

QY 9 VELPPREADTLAISRIPEVTCVVVDVSHEDPEVKFWWYDGVEVHNAKTRPREEGYNST 68

PLIEPPREADTLAISRIPEVTCVVVDVSHEDPEVTSWTRQNGEAVKTHTNISESHPNAT 425

QY 69 YRVVSUTLVLQDWLNGKEYKCKSNKALPATSTRAK 109

R 426 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK 466
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Search completed: June 21, 2002, 08:59:33 Job time: 1632 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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protein - protein search, using sw model ŏ June 21, 2002, 09:00:25 ; Search time 48.19 Seconds (without alignments) 87.579 Million cell updates/sec Run on:

US-09-674-857-9 582 Title: Perfect score: Sequence:

1 APPVAGPSVFLFPPKPKDTL......CKVSNKALPAPIEKTISKAK 109

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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### ALIGNMENTS

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**SQUENCE OF 1-325 (MYELOMA PROTEIN TIL).

**X MEDLINE-81007873; PubMed-6774012;

**MEDLINE-81007873; PubMed-6774012;

**A Wang A.-C., Tung E., Fudenberg H.H.;

**The primary structure of a human igG2 heavy chain: genetic,

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**I Immunol. 125:1048-1054(1980).

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**MEDLINE-80001357; PubMed-113060;

**A MEDLINE-80001357; PubMed-113060;

**A Connell G.E., Parr D.M., Hofmann T.;

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**A The amino acid sequences of the three heavy chain constant region domains of a human igG2 myeloma protein.";

**Can. J. Biochem. 57:758-767(1979).
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Krawinkel U., Rabbitte T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
                                                                                                                                                                                                                                                                               [1]
SEQUENCE OF 2-326 FROM N.A.
SEQUENCE OF 2-326 FROM N.A.
MEDLINE-82197621; PubMed-6804948;
Ellison J.W., Hood L.E.;
Ellison J.W., Hood L.E.;
"Linkage and sequence homology of two human immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECURINCE OF 238-275 (ZIE).
MEDLINE-80114419; PubMed=118920;
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SEQUENCE OF 88-115 FROM N.A.
MEDLINE=83001943; PubMed=6811139;
Takahashi N., Geda S., Obatea M., Nikaido T., Nakai S., Honjo 'Structure of human immunoglobulin gamma genes: implications evolution of a gene family.";
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                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                    326 AA
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SEQUENCE OF 99-177 AND 310-326 FROM N.A.
                                    PRT;
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IGHG2.
                                       STANDARD;
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                                GC2_HUMAN
P01859;
GC2_HUMAN
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111 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 170

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AT OR NEAR THE COMPLEMENT-BINDING SITE.
REMOVED POST-TRANSLATIONALLY (PROBABLE).
5 -> A (IN MYELDMA PROTEINS TIL & ZIE).
/FIId=VAR_003889.
C -> S (IN REF. 3).
8310878C6878CF9C CRC64;
                                                                                                                   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri "Characterization of the two unique human anti-flavin monoclonal
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003509; Ig_like.
Pfam: PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; FM00407; IGC1; 2.
RROSTIF; PS00290; IGC1; 2.
Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                           DISULPIDE BONDS.
MEDLINE-69064124; PubMed=5782707;
Franqione B. Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
                                                   Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
                                     REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
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HINGE.
                                                                                                                                               immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995).
                                                                                                        MEDLINE=95255298; PubMed=7737190;
                                                                                                                                                                               DISULFIDE BONDS.
MEDLINE=72033500; Pubmed=4940472;
immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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                                                                                          SEQUENCE OF 1-121 (DOT)
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HSSP; P01857; lFC1.
MIM; 147110; -.
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96.0%; Score 559; DB 1; Length 326; 94.5%; Pred. No. 4e-49; Live 4; Mismatches 2; Indels
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Conservative

Matches 103;

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Query Match Best Local Similarity

Amino SEQUENCE FROM N.A.
MEDLINE-82274238; PubMed-6287432;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
Nucleic Acids Res. 10:4071-4079(1982). "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; Biochemistry 9:3171-3181(1970). DISULFIDE BONDS.

MEDLINE=77070267; PubMed=1002129;

MEDLINE=77070267; PubMed=1002129;

MEDLINE=77070267; PubMed=1002129;

Preker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal 19G1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin 1gG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.;
The covalent structure of a human gamma G-immunoglobulin. VII. A acid sequence of heavy-chain cyanogen bromide fragments HI-H4."; Ponsting! H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymctryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.", MEDLINE-71064025; PubMed-5530842; Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., MEDLINE=71064027; PubMed=4923144; Gall W.E., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. X. 61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109 Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976). SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS. MEDLINE-83289131; Pubmed-6884994; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last Sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 330 AA SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). MEDLINE-71064024; Pubmed-5489771; PRT; SEQUENCE (MYELOMA PROTEIN NIE). MEDLINE-77070269; Pubmed=826475; Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970). Ig gamma-1 chain C region. IGHG1. STANDARD; SEQUENCE OF 136-329 (EU) Homo sapiens (Human) NCBI_TaxID=9606; DISULFIDE BONDS. Edelman G.M.; GC1_HUMAN P01857; SC1_HUMAN g ò

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                                                                        "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus and 2.8-a resolution.";

Blochemistry 20:3361-2370 [1981].

-! MISCELLANEONG: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKER, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.

-! MISCELLANEONG: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

-! MISCELLANEOUS: BU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155,156,177,195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
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R -> R (IN GIM(3) MARKER).

/FTId-VAR_003886.

D -> E (IN GIM(NON-1) MARKER).

/FTId-VAR_003887.

L -> M (IN GIM(NON-1) MARKER).

/FTId-VAR_003888.
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HEAVY CHAIN).
HEAVY CHAIN).
 Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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                              X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; PubMed=7236608;
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PIR; A02146; GHU.
PDB; 1FC1; 15-JUL-92.
PDB; 1FC2; 15-JUL-92.
MIM; 147100; -.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; Ig_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
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                                                               Deisenhofer J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDLINE=70207560; PubMed=419269;
MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-83157104; PubMed-6299662;
Ellison J.W., Buxbaum J.M., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
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36106 MW; 3770EE106C2FA33D CRC64;
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Pred. No. 5.1e-49;
1; Mismatches 1;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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PIR; A02150; G4HU.
HSSP; P01842; 7FAB.
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93.0%;
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Homo sapiens (Human).
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Prinary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO 12-97 OF PROTEIN WIS.
MEDLINE=77118561; PubMed=402363;
MIChaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of human 1gG3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Blol. Chem. 252:883-889(1977).
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21-JUL-1986 (Rel. 01, Last sequence update)
11-JUL-1986 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
1g gamma-3 chain C region (Heavy chain disease protein) (HDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC). MEDLINE=77021516; PubMed=823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.; Walfenstein acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                    INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                    INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                             Score 526; DB 1; Length 327;
Pred. No. 8.4e-46;
                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
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     290 AA
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MEDLINE-82247835; PubMed-6808505;
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MEDLINE-81021548; Pubmed-6774747;
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Best Local Similarity
Matches 98; Conserv
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MIM: 147130:
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                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
AND ALL OF THE CH1 REGION.
-!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL GAMMA-3 HEATY CHAINS.
-!- MISCELLANEOUS: DISEASE PROTEIN OWM MAY REPRESENT AN ALLELIC FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain; Immunoglobulin C region; Glycoprotein; Repeat.
                                                                                                               gene deletion model.";
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR ANOTHER GAMMA CHAIN SUBCLASS.

MISCELLANGOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
Alexander A., Steinmetz M., Barritault D., Frangione B., Franklin E.C., Hood L., Buxbaum J.N.; "Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIMER).
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/FTId=VAR_003890.
/FTId=VAR_003891.
/FTId=VAR_003891.
F -> Y (IN OMM).
/FTIG=VAR_003892.
/FTIG=VAR_003893.
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CH3.
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PIR; A02149; G3HUWI.
HSSP; P01857; 1FC1.
MIM; 147120; -
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Interpro: IPR003507; Ig_cl.
Interpro: IPR003507; Ig_cl.
Ffam: PF00047; Ig; 2.
SMART: SMO0410; Ig_like; 1.
SMART: SMO0407; IGcl: 1.
PROSITE: PS00290; IG_MHC; 1.
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MEDLINE-89232738; PubMed-3149946;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 3. SMART; SM00410; IG_like; 1. SMART; SM00407; IGcl; 2. PROSITE; PS00290; IG_MHC; 1.
                   13 INBRED GUINEA PIGS.
PIR; A02151; G2GP.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                             Best_Local Similarity 73.6%
Matches 81; Conservative
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GCB_RAT
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MEDLINE=71058486; PubMed=5538616;
Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISOLITE SOUND:
MEDLINE-7105847:
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                         MEDILNE-71058471; PubMed-5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
Structure of heavy chain from strain 13 quinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
Biochemistry 10:18-25(1971).
                                                                                                            Gaps
                                                                                                                                4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2 chain C region.
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                        Length 290;
                                                                                                           Indels
S -> N (IN OMM).
/FTDIG-VAR_003894.
MISSING (IN LOUC).
/FTIG-VAR_003895.
F -> Y (IN OMM).
/FTIG-VAR_003896.
                                                                                                                                                                     Query Match 89.2%; Score 519; DB 1; L
Best Local Similarity 89.6%; Pred. No. 3.7e-45;
Matches 95; Conservative 8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                             Trischmann T.M.;
Submitted (APR-1975) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 227-311.
MEDLINE-75036073; PubMed-4609467; Trischmann T.M., Cebra J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 134-226.
MEDLINE-75036072; PubMed-4429665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 13:4796-4803(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iochemistry 13:4804-4811(1974)
                                                           290 AA; 32331 MW;
                                                                                                                                                                                                                                          STANDARD;
                    227
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 4-68.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10141;
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                    227
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P01862;
                                                           SEQUENCE
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GC2_CAVPO
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Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
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"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74.473-482(1988).
PIR; PS0018; PS0018.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PP--VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN).
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CHAIN).
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InterPro; IPR003507; Ig_c1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Ig_; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.2%; Score 432; DB 1; Length 329; 73.6%; Pred. No. 2.5e-36; ive 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36074 MW; 5D231B7164D1FBA9 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2B chain C region.
Rattus norvegicus (Rat)
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PIR; A02161; GHRB.
HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
                                                                                                                                                                                                                                                                                                                                                             35404 MW;
                                                                                                Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 71.00
The Tay Conservative
                                      EMBL; M16426; AAA31289.1;
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                                                                                                                                                                                                                                                                                                                                                            323 AA;
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P22436;
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MEDLINE-76135469; PubMed=1243651;

Pratt D.M., Mole L.E.;
"Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
                                                                                                                          Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit 1gG heavy chain from the recombinant
                                                                                       Gaps
                                                                                                              4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKERS AND REF.5 THE E15 MARKER.
                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculús (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell, Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-70110015; PubMed-5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit
immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a cDNA encoding
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MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding
heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                             DB 1; Length 333;
                                                                                    11; Indels
                                                                                                                                                                           181 QYNSTFRVVSALPIQHQDWASGKEFKCKVNNKALPSPIEKTISKPK 226
                                                                                                                                                             64 OYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
                        55F8B64D48D460A6 CRC64;
                                                            73.7%; Score 429; DB 1
70.8%; Pred. No. 5e-36;
                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                  323 AA
                                                                                    20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84030930; PubMed-6313520;
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                        36497 MW;
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                                                                                    Conservative
                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                            gamma chain C region.
147
253
333 AA;
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                                                                         Best_Local Similarity
Matches 75; Conserv
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P01870;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                               IN REF. 2).
REF. 3 AND 4).
REF. 5).
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E15 MARKER).
REF. 2).
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                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region.
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine 19G3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                     InterPro; IPR003505; Ig_MHC.
InterPro; IPR003507; Ig_c1.
InterPro; IPR0035005; Ig_like.
InterPro; IPR0036005; Ig_like.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGCl; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Iransmembrane; Alternative splicing.
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MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                              Length 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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36228 MW; F45827174182BAD6 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-3 chain C region, membrane-bound form.
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EMBL; V01285; CAA24767.1; ALT_SEQ.
PIR: AQ2155; GBNSM.
HSSP; P01857; IFC1.
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223
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                   PIR; B02156; G3MSC
HSSP; P01857; 1FC1
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J00451;
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MEDILINE-80012837; PubMed-113776;
ROGETS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Saldman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Ig_like; 1.
SMART; SM00407; IG_like; 1.
SMART; SM00407; IG_like; 1.
Immunoqlobulin domain; Immunoqlobuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.1%; Score 425.5; DB 1; Length 398; Best Local Similarity 70.3%; Pred. No. 1.4e-35; Matches 78; Conservative 14; Mismatches 16; Indels 3
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region.
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CYTOPLASMIC
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MEDLINE-78242288; Pubmed-98524;
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Cell 18:559-568(1979).
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                        DISULFIDE BONDS (MOPC 21).
MEDLINE-73008889; PubMed-5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Adetugbo K.; "Evolution of immunoglobulin subclasses. Primary structure of
                                                                                                                                                                                                                                                                                                                           CHAIN).
CHAIN).
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                                                                                                                                                                                                                                                                                                                                          CHAIN).
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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               murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                     EMBL; A02159; GINS:
HSSP, P01842; 7FAB.
GlyCoSuiteDB; P01868;
MGD, MGI: 96446; 19h-4.
InterPro; 1PR00306; 1g_MHC.
InterPro; IPR003597; 1g_C1.
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ID GCIM_MOUSE STANDARD;
AC PO1869;
DT 21-JUL-1986 (Rel. 01, Created)
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MEDLINE-8222190; PubMed-6283537;
Yamawaki-Katekoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Katekoka Y., Nakai S., Miyata T., Honjo T.;
Nuclectide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOWOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O., "MRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 323-366 FROM N.A. MEDIINE-82115295; PubMed-6799207; Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Elsenberg D., Wall R.; "Gene segments encoding transmembrane carboxyl termini of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH1.
HINGE.
CH2.
CH3.
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EMBL; V00793; CAA24173.1; -.
PIR; B02159; CAA24174.1; -.
PIR; B02159; GIMSM.
HSSP; P01842; 7FAB.
INTERPO; IPR003066; I9_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin gamma chains.";
Cell 26:19-27(1981).
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IGc1; 2.
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217
324
82
102
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                          Mus musculus (Mouse).
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                                                                                                                                                                     Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                          Gaps
                                                                                                                                                             SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 67
                                                                                                                                                                                                                                                                                                                                                                                                       Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.; "Sequence of a rat immunoglobulin gamma 2c heavy chain constant region CDNA: extensive homology to mouse gamma 3."; Eur. J. Immunol. 18:317-319(1988).
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       INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                    Length 393;
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                                                                           CYTOPLASMIC (POTENTIAL).
4CC88343B7A1CE27 CRC64;
                                              N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                             68 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                  70.6%; Score 411; DB 1; Le
70.6%; Pred. No. 3.9e-34;
Live 18; Mismatches 12;
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                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2c chain C region.
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                                                                  POTENTIAL.
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HINGE.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3
SMART; SM04010; IG_like; 1.
SMART; SM0407; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                      43386
                                                                                                                  Query Match 70.65
Best Local Similarity 70.65
Matches 72; Conservative
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                                                                                                                                                                                                                                                          120 PSVFIFPPKRKDILMITLTPKVTCVVVDVSEEEPDVQFSWFVDNVRVFTAQTQPHEEQLN 179
                                                                                                                                                                          Gaps
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"Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6;
MEDLINE=82037861; PubMed=6170065;
SChreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
"Multiple differences between the nucleic acid sequences of the
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                                                                                                               DB 1; Length 329
                                                                                                                                                                       15; Indels
                             36571 MW; 5FCD7B7933850773 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                             67 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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                                                                                                               68.0%; Score 396; DB 1 68.0%; Pred. No. 1e-32;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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PIR; A02153; G2MSAB.
HSSP: P01875, 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_Like.
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SMART; SM00410; iG_like; 1.
SMART; SM00407; IGCl; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                       Conservative
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Best Local Similarity
Thes 72; Conserva
249
329 AA;
                                                                                                                                          Best Local Similarity
Matches 70; Conserv
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GCAB_MOUSE
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musculus (Mouse)
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            115 PPCAAPDLLGGPSVFIFPPKIKDVLAISLSPAVTCVVVDVSEDDPDVQISWFVNNVEVHT 174
                                                                                                                                                                                                  Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                    Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 SVFLFPPKPRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 67
      PPVA-----GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
013BAB45EF49B9DA CRC64;
                                     AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
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HEAVY CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 389; DB 1; Length 326;
; Pred. No. 5.2e-32;
18; Mismatches 14; Indole
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                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-1 chain C region.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -JUL-1986 (Rel. 01, Created)
-JUL-1986 (Rel. 01, Last sequence update)
-MAY-2000 (Rel. 39, Last annotation update)
gamma-2A chain C region, A allele.
                                                                                                                                                                                                                                                                                                                                                                                                                             66.8%; Score 389;
68.0%; Pred. No. 5.
                                                                                                                                                                                                                                                                                                     CH1.
HINGE.
                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed-3149946;
                                                                                                                                                                                                                                                                                                                                                                                                    35946 MW;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                    Gene 74:473-482(1988).
PIR; PS0017; PS0017.
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220
220
27
102
106
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326 AA;
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                                                                                                                                                                     NCBI_TaxID=10116;
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21 JUL-1986 (
30-MAY-2000 (
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P01863;
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GCAA_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                  Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-81223894; PubMed-6787604;
Ollo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic family.";
Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
                                                                                                                                                            MEDLINE-81076554; PubMed-6777755; Sikorav J.-L., Auffray C., Rougeon F.; Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA."; Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
Eukaryota; Metazoa; Chordata; Craniata; Verceusaca, curinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       de Preval C., Fougereau M.; "Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges."; Eur. J. Blochem. 30:452-462(1972).
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SMART; SM00407; IGG1; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-81198976; PubMed-6262729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYELOMA PROTEIN MOPC 173.
MEDLINE=74175517; PubMed=4831970;
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HSSP; P01842; 7FAB.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
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250
330
330 AA;
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                                                                  NCBI_TaxID=10090;
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SEQUENCE F
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Ouery Match 66.5%; Score 387; DB 1; Length 330;
Best Local Similarity 66.0%; Pred. No. 8.4e-32;
Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps
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δy	4 VAGPSVFLFPPRKRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63	63
qq	118 LGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRE 177	17
ĉ	64 OVNSTRVBIGNT HOT HODBIT NOVEVNOVISONVI BABITERAT SENAV 100	

Search completed: June 21, 2002, 09:00:26 Job time: 1450 sec

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June 21, 2002, 08:37:55 ; Search time 102.05 Seconds (without alignments) 102.633 Million cell updates/sec Run on:

1 APPVAGPSVFLFPPKPKDTL......CKVSNKALPAPIEKTISKAK 109 US-09-674-857-9 582 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:* ..... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARTES

	Description	q qamma chain C	q qamma-2 chain	amma-1	g gamma-1 chain	g heavy chain V	g gamma-3 chain	g gamma-3 chain	g gamma-4 chain	ь	g gamma 2b	ь	Б	g gamma 3	6	g heavy ch	g gamma-2 cha:	g gamma-2b	6	g gamma-3	g gamma-	Ig heavy chain C r	Б	6	q qamma-1 chain	o.	gamma-2	gamma-2c	ď		
SUMMARIES	Œ		G2HU	S31866	Снно	869339	A60764	A23511	G4 HU	G3HUWI	147160	147159	147162	147161	147158	S22080	G2GP	PS0018	GHRB	G3MSC	G3MSM	C30554	S31459	G1MS	G1MSM	PC4436	S06611	S00847	G2MSAB	PS0017	
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Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma heavy cha	Ig gamma-1 chain C	Ig epsilon-chain -	Ig epsilon chain C	Ig heavy chain pre	Ig epsilon chain C
G2MSA	S37483	G2MSBM	G2MS11	S01321	S40295	PS0019	B30503	A30503	146732	S14236	I36948	ЕННО	S04845	EHRT
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330	469	405	474	475	446	322	112	88	180	152	426	428	549	429
66.5	66.5	66.3	66.3	64.9	64.8	8.09	54.8	47.3	45.4	30.4	28.4	28.3	27.7	27.5
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### ALIGNMENTS

Jul-1999

RESULT PT0207 Ig gam CJ Spec CJ Spec CJ Acce CJ Acce CJ Acce AJ TELI AJ REFE AJ Acce AJ ACce AD ACce AJ ACce AD ACce A	RESULT 1  Ig gamma chain C region - chimpanzee C; Species: Pan troglodytes (chimpanzee) C; Chate: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999 C; Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999 C; Chacession: Pr0207 R; Ehrlich, P. H.: Moustafa, Z. A.; Oestberg, L. Mol. Immunol. 28, 319-322, 1991 A; Aitle: Nucleotide sequence of chimpanzee Fc and hinge regions. A; Reference number: Pr0207; MUID:91287716 A; Accession: Pr0207 A; Accession: Pr0207 A; Residues: 1-234 cEHR> C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Reywords: immunoglobulin F; 48-117/Domain: immunoglobulin homology <imm></imm>
Que Bes Mat	Query Match 96.2%; Score 560; DB 2; Length 234; Best Local Similarity 93.9%; Pred. No. 1.9e-49; Matches 107; Conservative 0; Mismatches 1; Indels 6; Gaps
Qy Db	2 PPVAGPSYFLFPPRENDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHN 55
oy D	56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109 

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R;Filpula, D. submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene produc A;Reference number: S31866
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Cispecies: Homo sapiens (man)
Cispecies: Ann-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
Ciscossion, A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
Fillison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                          A; Cross-references: EMBL: X70421; NID: 933068; PIDN: CAA49866.1; PID: 933069
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9
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F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                              Length 255;
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93.0%; Pred. No. 3.3e-49;
iive 1; Mismatches 1.
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Best Local Similarity 93.09
Matches 106; Conservative
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A; Molecule type: mRNA
A; Residues: 1-255 <FIL>
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A; Motecule vype: protein
A; Motecule vype: protein
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A; Motecule vype: protein
A; Note: Trp-156 is at or near the complement-binding site
A; Note: Trp-156 is at or near the complement-binding site
Can. J. Biochem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of a A; Reference number: A90752; MUD: 80001357
A; Motecule vype: protein Zie
A; Mocecasion: A90752
A; Motecule vype: protein
A; Mocecale vype: protein
A; Motecule vype: protein
A; Motecale vype: protein
A; Motecaner annober: A93132; MUD: 80114419
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A; Motecule vype: protein
A; Motecule number: A94591
A; Motecule vype: protein
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A.Note: Hodo sapiens (man) gene engineered and expressed in Escherichia coli
C.Date: 06-Jan.1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C.Accession: S31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RiMilstein, C.; Frangione, B.
Blochem. J. 121, 217-225, 1971
AyTitle: Disulphide bridges of the heavy chain of human immunoglobulin G2.
AyTitle: Disulphide bridges of the heavy chain of human immunoglobulin G2.
AyReference number: A00253; MID:72033500
AyReference number: Milstein, C.; Pink, J.R.L.
AyReference B.; Milstein, C.; Pink, J.R.L.
AyReference number: A93157; MID:69064124
AyReference number: A93157; MID:69064124
AyContents: annotation; Sa, disulfide bonds
AyGene: GBBIGHG2
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96.0%; Score 559; DB 1; Length 326;
Best Local Similarity 94.5%; Pred. No. 3.5e-49;
Matches 103; Conservative 4; Mismatches 2; Indels
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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A21511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Tille: Sequence of a human immunosolobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        u) with an IGHG4 conv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tig gamma-3 chain C region, form LAT - human Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cidacession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 AKTRPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267
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                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords immunoglobulin F;20-85/nomain:
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Pred. No. 5.3e-49;
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                                                                                                                                        A,Cross-references: EMBL:X81695
R;Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
A;Reference number: $72664
A;Accession: $72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 5.36
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keywords: İmmunoglobulin
20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A60764; MUID: 90007613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.9%;
93.0%;
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Best Local Similarity 94.3%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                 A; Molecule type: mRNA
A; Residues: 1-374 <KHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-377 <HUC>
                                                                                                                                                                                                                                                                                                               A; Status: preliminary A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                    A;Accession: S69339
A;Status: preliminary
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A; Molecule type: DNA
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A60764
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A23511
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                                                                                                                                                         Affitte: In Primacestruktur eines monoklonalen igdl-Immunglobulins (Wyelomprotein Nie), Affitte: Akzeestonen under: Agi668; WID: 7070269
A. Accession: B9168 and protein Nie
A. Mocule type: protein
A. Mesidues: 1-34, 0.76-96, KV, 98-115, 0.717-197, DV, 199-238, DV, 240, IV, 242-268, EV, 27
A. Mocule type: protein
A. McDerell and A. Molecule type: protein
A. Accession: Agi723
A. McDerell and A. Accession: Agi723
A. McDerell and A. Accession: Agi723
A. McDerell and A. Accession: Agi723
A. Accession: Agi723
A. McDerell and A. Accession: Agi723
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A. Accession: Agi723
A. Acc
A;Residues: '136-154,'O',156-165,'O',167-176,'O',178-194,'N',196-197,'D',199-238,'E',240,'A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
F; ponsting1, H: Hischmann, W.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 heavy chain V region precursor - human
C;Species: Homo saplens (man)
C;Daces: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S63339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Blochem. 229, 54-66, 1995
A;Fitle: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
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175 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220
                                                                                                                                                                                                                Ig gamma-3 heavy chain disease proteins - human
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C; Species: Homo sapiens (man)
C; Species: Assequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C; Accession: A90933; A90249; A002150
BNA 1, 11-18, 1981
A; Tille: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A; Reference number: A90933; MUID:83157104
A; Reference number: A90933; MUID:83157104
A; Residues: 1-327 < ELL.)
A; Residues: 1-327 < ELL.)
A; Residues: L; Buttery, S.H.; De Vries, G.M.; Milstein, C.
B; Dochem. J. 117, 33-47, 1970
A; Reference number: A90249; MUID:70207560
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant IA; Residues: 1-30;81-326 < PIN>
A; Residues: 1-30;81-326 < PIN>
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A90249
A; Circos-references: GDB:119340; OMIM:147130
A; Multiplication: 14932.33-149422.33
A; Dittiplication: 14932.33-149422.33
A; Dittiplication: Jayara (region; immunoglobulin heterotetramer; immunoglobulin c; Reywords: duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; duplication; homology ximi.
F; 39-110/Region: hinge
F; 134-213/Demain: immunoglobulin homology ximi.
F; 134-213/Demain: immunoglobulin homology ximi.
F; 134-213/Demain: immunoglobulin homology ximi.
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:9577056
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                          A/Gene: GDB:IGHG3
A/Cross-references: GDB:119339; OMIM:147120
A/Map position: 1492.33
A/Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C/Superfamily: immunoglobulin C region; immunoglobulin homology C/Keywords: immunoglobulin homiology <IMM>
                                                                                                                                                                                                                                                                                                                                                      Length 377;
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                                                                                                                                                                                                                                                                                                                                       92.6%; Score 539; DB 2; Length 37
ilarity 94.3%; Pred. No. 4.5e-47;
Conservative 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.4%; Score 526; DB 1, 92.5%; Pred. No. 8e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - human
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C;Species: Homo sapiens (m
                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Matches 100;
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Best Local Simi
Matches 98;
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                        C; Genetics
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G4HU
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4 WAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE, 63

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A. Wolfensteiner at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in B. Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, B.C.
B. Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, B.C.
A. Wolfenstein Blophys. Res. Commun. 71, 907-914, 1976
A. Reference number: A90198; WUID: 77021516
A. Contents: Neavy chain disease protein Zuc, partial sequence corresponding to residu A. Accession: A90198
A. Molecule type: protein
A. Residues: 59-125, 'E8', 128-226, 228-289 < WOL>
A. Note: this protein lacks most of the V region, all of the CHI region, and part of the R. Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, A. Reference number: A93915; MUID: 82247835
A. Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletine A. Rochents: heavy chain disease protein Omm
A. Residues: 12-70315.
A. Molecule type: mRNA
A. Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-A. Note: a removed nonetherer and a removed 
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92219; A90198; A93915; A02149
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser. E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea
A;Reference number: A90442; MUID:81021548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Readues: 1-289 <FRA>
A,Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A,Note: this protein lacks most of the V region and all of the CH1 region. Residue 12
A,Note: the sequence of residues 42-76 was taken from the reference that follows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A: Title: Primary structure of the 'hinge' region of human 1gG3. Probable quadruplicat
A: Reference number: A92219; MUID: 77118561
A: Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: a carboxyl-terminal Lys is removed posttranslationally A; Note: this sequence may represent an allelic form or another gamma chain subclass C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A92219
A; Molecule type: protein
A; Residues: 12-97 < MIC>
A; Note: the hinge region in gamma-3 chains is about four times as long as in other
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C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F; 203-270/Domain: immunoglobulin homology <IMM>F; 203-270/Domain: immunoglobulin homology <IMM>F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 6, 140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: heavy chain disease protein Wis A; Accession: A90442
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A,Gene: GDB:IGHG3
A,Cross-references: GDB:119339; OMIM:147120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Best Local Sim
Matches 95;
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Ig gamma 4 chain constant region - pig (fragment)
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C.Accession: I47162
J. Immunol: 153, 3565-3573, 1994
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A.Reference number: I47158; MUID:95015845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 21-reb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3373, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: I47158; MUID:95015845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1.328 <KAC>
A; Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
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Pred. No. 1.6e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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79.88;
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C;Superfamily: immunoglobulin C
F;82-151/Domain: immunoglobulin
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Best Local Similarity 79.8
Matches 83; Conservative
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Best Local $
                                                                                                                                                                                                                                                                                                            C; Genetics
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C;Species: Sus scrofa domestica (domestic pig)
C;Accession: 17Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
R;Kacskovics, I: Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a S,Reference number: 147159
A;Tetle: Five putative subclasses of swine IgG identified from the cDNA sequences of a S,Reference number: 147159
A;Reference number: 147159
A;Reference number: 147159
A;Residues: 1-328 «KAC>
A;Coss-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics: 19G2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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66 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 80.4%; Score 468; DB 2; Le
1 Similarity 80.8%; Pred. No. 6.3e-40;
84; Conservative 13; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.4%; Score 468; DB 2; L
80.8%; Pred. No. 6.3e-40;
iive 13; Mismatches 7;
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Best Local Similarity 80.8
Matches 84; Conservative
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Matches 84; Conserv
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RESULT 11 147159

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Query Match

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Search completed: June 21, 2002, 08:37:55 Job time: 429 sec
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19 heavy chain precursor (B/WT.4A.17.H5.A5) - bovine

19 heavy chain precursor (B/WT.4A.17.H5.A5) - bovine

N.Alternate names: 19 gamma-1 chain or region (clone 8.10)

C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

R; Sanders, P.G.

A; Recreated to the EMBL Data Library, November 1991

A; Recuelle type: mRNA

A; Residues: 1-470 < SAN>

A; Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440

A; Residues: 1-470 < SAN>

A; Residues: 1-470 < SAN>

A; Recession: S06610; MUID:90097956

A; Molecule type: DNA

A; Residues: 142-470 < SYN>

A; Cross-references: EMBL:X16701

A; Note: the sequence was determined from the germline gene
R;Kacskovics, I.; Sun, J.; Butler, J.E.
A; Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the CDNA sequences of a;
A;Title: Five putative subclasses of swine IgG identified from the CDNA sequences of a;
A;Reference number: I47158; MUID:95015845
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: I-328 <ARC>
A;Cross: references: EMBL:U03778; NID:9433121; PIDN:AAA52216.1; PID:9433122
C;Genetics:
A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <INM>
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A.Introns: 98/1: 111/1; 221/1
G.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Superfamily: immunoglobulin heterotetramer; immunoglobulin; membrane protein
F.161-225/Domain: immunoglobulin homology <IMM>
F.181-235/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.7%; Score 452; DB 2;
79.0%; Pred. No. 2.6e-38;
tive 12; Mismatches 10
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72.7%; Pred. No. 2.7e-36;
tive 11; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity 72.79
Matches 80; Conservative
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Best Local Similarity
Matches 83; Conserv
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Sequence 90, Application US/09485737B
Patent No. 6350860
GENERAL INFORMATION:
APPLICANT: BHyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-485-737B-90
                                                                                                                                                                                                                                                                                                                                                        US-09-485-737B-67
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SEQ ID NO 67
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 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 67,
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Sequence 21,
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Sequence 4,
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/RB_COMB.pep:*
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Compugen Ltd
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US-08-232-539D-55
US-08-430-633-4
US-08-620-694A-4
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US-08-284-391B-33
US-09-218-950-33
US-09-178-869-4
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US-09-180-100-11
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US-09-022-696-4
US-09-022-253-4
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               GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Sablon, Enter any applicant: Sablon, Enter Enter any applicant: Sablon, Enter E
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Pred. No. 6.6e-61;
1; Mismatches 1; Indels
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US-08-236-311-7

US-08-180-100-22

US-09-180-100-22

US-09-131-247-16

US-09-131-247-14

US-09-131-247-14

US-09-133-593A-8

US-09-176-228-3

US-09-33-593A-8

PCT-US95-03866-12

PCT-US95-03866-14

PCT-US95-03866-14

PCT-US95-03866-14

US-08-397-411-7

US-08-397-411-7

US-08-895-538
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APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
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Best Local Similarity 98.2
Matches 108; Conservative
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97.6%;
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Best Local Similarity 97.39
Matches 107; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        HOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-444-644-21
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Patent No. 6015555

GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: CONJUGATES
TITLE OF INVENTION: CONJUGATES
CORRESPONDENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitan Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS; FILE REFREENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION WINBER: POGY/EP 98/05165
PRIOR PLILING DATE: 1998-08-18
PRIOR PLILING DATE: 1998-06-18
SPRIOR PLILING DATE: 1997-08-18
SOFTWARE: PATENTING DATE: 1997-08-18
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 576; DB 4;
Pred. No. 1.2e-60;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-UUL-1994
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
ATCHNEY, GENT INFORMATION:
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98.2%;
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Best Local Similarity 98.23
Matches 108; Conservative
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MEDIUM TYPE: Floppy
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STATE: MA
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US-08-444-644-21
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**RESERVATION NUMBER: 34.40

**RESITRATION NUMBER: 4.1.64

**RESITRATION NUMBER: 6.1.64

**RESITRATION NUMBER: 7.1.64

**RESITRATIO
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                                                                                                                                                                                                                                     APPLICANT: ALDERSON, MARK
APPLICANT: ARMITAGE, RICHARD
APPLICANT: COMEAU, JEFFREY
APPLICANT: COMEAU, MICHAEL
APPLICANT: FARRAH, THERESA
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SPRIGGS, MELANIE
ISOLAGE INVENTION: That Bind MHC Class II Beta Chains
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                                             61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                  66 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 115
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Pred. No. 9.1e-61;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION System 7.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,633
FILING DATE: 28-APR-1995
RIOR APPLICATION:
435
APPTICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,397
FILING DATE: 04/28/94
ATTORNEY ABENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            E: IMMUNEX CORPORATION 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                            ; Sequence 4, Application US/08430633; Patent No. 5726286; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.6%;
Best Local Similarity 97.3%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: SEATTLE STATE: WASTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: 1961 FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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US-08-430-633-4
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                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                          Score 571; DB 4; Length 110;
Pred. No. 3.8e-61;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                           61 PREEQINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 571; DB 2;
Pred. No. 4e-61;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 55, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 1GE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 21 Apr. 1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-JAN 1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTONNEY/AGENT INPORMATION:
NAME: SVODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/POCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genemiech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
                                                                                                                                                            Query Match 97.6%;
Best Local Similarity 97.3%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.6%;
Best Local Similarity 97.3%;
Matches 107; Conservative
: 110 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
                                                      ; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-232-246A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650/952-9881
                                             linear
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                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Yao, Zhengbin
APPLICANT: Sprigs, Melanie
APPLICANT: Eanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: S1 University Street
CITY: Seattle
STATE: Wa
COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MICTOSOFT WORD for Apple, Version 6.0.1
APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 23 MARCH 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/COKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
NAME: PERKINS, PATRICIA Anne
REGISTRATION NUMBER: 24,695
REFERENCE/COKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (266)587-0430
                         ; Sequence 4, Application US/08620694A; Patent No. 5869286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08936854; Patent No. 5925734; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONGANISM: Human
IMMEDIATE SOURCE:
CLONE: IGG1 FC
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.08-620-694A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-620-694A-4
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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APPLICANT: COMEAU, JEFFREY
APPLICANT: COMEAU, MICHAEL
APPLICANT: CARRAH, THERESA
APPLICANT: SFRIGGS, MELANIE
TITLE OF INVENTION: ISOlated Epstein-Barr Virus BZLF2 Proteins
TITLE OF INVENTION: That Bind MHC Class II Beta Chains
NUMBER OF SEQUENCES:
ADDRESSEE: IMMUNEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09022255
Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yeo, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.6%; Score 571; DB 2; Length 212; 97.3%; Pred. No. 9.1e-61; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Apple Operating System 7.1 SOFTWARE: Microsoft Word for Apple, Version 5.1a APPLICATION DATA: APPLICATION NUMBER: US/08/936,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,633
FILING DATE: 28-APR-1995
APPLICATION NUMBER: 08/235,397
FILING DATE: 04/28/94
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
RESISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2612
TELECOMMUNICATION INFORMATION:
mediatron...
                                                                                                                                                                                                                             ADDRESSEE: IMMUNEX CORPORATION STREET: $1 UNIVERSITY STREET CITY: SEATTLE STATE: WASHINGTON COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206)587-0430
TELEPAX: (206)587-0430
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGIALAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.6
Best Local Similarity 97.3
Matches 107; Conservative
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CLONE: IGG1 FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-936-854-4
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US-09-022-255-4
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MOLECULE TYPE: protein ORIGINAL SOURCE:
                                         COMPUTER READABLE FORM:
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ADDRESSEE: Immunex C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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STREET: Die
TTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-022-253-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.6%; Score 571; DB 3; Length 212; Best Local Similarity 97.3%; Pred. No. 9.1e-61; Matches 107; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/022,255
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
ATTONNEY,AGENT INFORMATION:
NAME: PERKINS, PARTICIA ANDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                   E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-022-696-4
; Sequence 4, Application US/09022696
; Patent No. 6072037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein ORIGINAL SOURCE:
CORRESPONDENCE ADDRESS:
                                                                                                               ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: 1961 FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (206)
                                                         Seattle
                                                                                                                                                                                                                                                                         FILING DATE:
                   ADDRESSEE:
                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-022-255-4
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COMPUTER READABLE FORM:
WEDIOM TYPE: Floppy disk
COMPUTER ADABLE FORM:
WEDIOM TYPE: Floppy disk
COMPUTER: ADABLE FORM:
WEDIOM TYPE: Floppy disk
COMPUTER: ADABLE FORM:
CURSETTOR ADABLE STETMEN ADABLE FORM:
CURSETTOR ADABLE ADABLE FORM:
FRICK APPLICATION NUMBER: US/09/022,696
FILLING DATE: 34 MACH 1995
CLASSIFTORTION NUMBER: US/09/022,696
FILLING DATE: 33 MACH 1995
CLASSIFTORTION NUMBER: 34,695
FILLING DATE: 33 MACH 1995
CLASSIFTORTION NUMBER: 34,695
FILLING DATE: 34 MACH 1995
CLASSIFTORTION NUMBER: 34,695
FILLING DATE: 34,695
FIL
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: __...oukESS:
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
        APPLICATION NUMBER: US/09/022,260
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFCATION:
PRICH APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acid
STRANDENESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.6%;
Best Local Similarity 97.3%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
CLONE: 1961 FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-022-260-4
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Sequence 4, Application US/09022260

Sequence 4, Application US/09022260

Sequence 4, Application US/09022260

Settle 6100235

APPLICANT: Vao, Zhengbin

APPLICANT: Spriggs, Melanie

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 9.1e-61;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: Apple Operating System 7.5.5 Microsoft Word for Apple, Version 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
CCMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                        FILING DAIE.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
TITING DATE: 7 AUGUST 1995
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 6096305 Relevant
                                                           US/09/022, 253
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.6%;
Best Local Similarity 97.3%;
Matches 107; Conservative
                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IgG1 Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-022-253-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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Gaps
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APPLICANT: Sprigss, Melanie
APPLICANT: Sprigss, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                       61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                               74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
       Length 212;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
Score 571; DB 3; L. pred. No. 9.1e-61; 1; Mismatches 2;
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.6%; Score 571; DB 4; Length 212; 97.3%; Pred. No. 9.1e-61; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/COOKET NUMBER: SGAR-00371
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
worm: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPRIL CANTE SCARLATO, GREGORY D.

TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                 ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
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US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
                                                                                                                                              Indexion (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

CORIGINAL SOURCE:

MORGANISM: Human

IMMEDIATE SOURCE:

CLONE: IGG1 FC

US-09-022-257-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.6
Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-595-043A-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTY: USA
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
FITING NAME: US/09/022,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.6%; Score 571; DB 4; Best Local Similarity 97.3%; Pred. No. 9.1e-61; Matches 107; Conservative 1; Mismatches 2;
                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Paricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09022257
Patent No. 6197525
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
CLONE: IGG1 FC
FILENG DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us-09-022-259-4
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Gaps

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us-09-674-857-8.rai
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                  Gaps
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                                                                    Query Match

97.6%; Score 571; DB 2; Length 232;
Best Local Similarity 97.3%; Pred. No. 1e-60;
Matches 107; Conservative 1; Mismatches 2; Indels
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Dp
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Search completed: June 21, 2002, 08:32:16 Job time: 90 sec

Fri

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June 21, 2002, 08:36:08; Search time 224.82 Seconds (without alignments) 54.346 Million cell updates/sec
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1 APELLGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                   747574
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                 Run on:
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121: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
122: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:* 14: 115: 116: 118: 120: 120: 120:

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
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7	576	98.5	-	20	AAW85692	MoTAbil fusion pro
m	571	97.6		13	AAR27680	Human immunoglobul
4	571	97.6		14	AAR41684	Undefined ORF2 enc
5	571	97.6		20	AAY42621	Human IqG1 Fcqamma
9	571	97.6		16	AAR87023	Immunoqlobulin G1
7	571	97.6	212	17	AAR97264	Human immunoglobul
æ	571	97.6		17	AAW02305	Human IqG1 Fc reqi
σ	571	97.6		19	AAW47354	Human immunoglobul
10	571	97.6		20	AAY23637	IgG1 Fc protein us
11	571	97.6		20	AAW92411	Human IgG1 Fc prot

25-FEB-1999.

Human IgG1 Fc regi Human immunoglobul Human immunoglobul Fc region of human Fc region of human Human immunoglobul	Native IgG Fc regi Native IgG Fc regi Human IgG Fc 1 all Human IgG Ron-A F Human IgG1 non-A F Human IgG1 A allot Sequence of human Tmmnnoglobulin G F	Human 1961 Fc prot Human 1961 Fc chai Human 1961 Fc chai Human 1961 hinge/F Human 1962 munoglobul Human 1mmunoglobul Human 1mmunoglobul Human 1mmunoglobul	Human partial 1961 Human immunoglobin Human FC (1961). Amino acid sequenc Human 1961 FC regil FC-MMP inhibitor f FC-MP protein seq TMP-FC protein seq FC-TNF-alpha inhibito FC-TNF-alpha inhibito	
AAY99937 AAY97182 AAY97250 AAB03809 AAB62062	AAB07474 AAB07475 AAB67201 AAB67202 AAB76421 AAB76422 AAP70173	AABL6955 AAY96529 AAW96953 AAW2632 AABS8690 AAY95579 AAY70251 AAG02642	AAY (7.915 AAB00897 AAB49155 AAY06617 AAY01372 AAB11958 AAB11958 AAB17951 AAB17951	
22 22 22 23 25 25 25 27		2222222	222222222222222222222222222222222222222	
, 212 212 212 212 212	218 218 218 218 228 224		22222222222222222222222222222222222222	
			0.7.7.00 0.7.7.00 0.7.7.00 0.7.7.00 0.7.7.00 0.7.00	
571 571 571 571 571 571	571 571 571 571 571	172 172 172 173 173 173 173 173	571 571 571 571 571 571 571 571	
12 13 14 15 17	118 22 22 24 25 25 26 27	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	

## ALIGNMENTS

AAW85689 standard; Protein; 468 AA.

AAW85689

127

RESULT

A_Geneseq_032802:*

Database :

AAW85689;

```
Antibody; humanised; variable region; heavy chain; light chain; interferon gamma; IFN; treatment; prevention; septic shock; cachexia; immune disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv; multivalent; ruminant.
                                                                                                                                                                                                                     oę
                                                                                                                                                                                                                                                    /note= "Human IgG1 heavy chain constant domain"
                                                                                                                                                                                          1.27
21.137
/note= "Humanised heavy chain variable domain
/BDD10"
                                                                                                                                                                                                                                                                        /note= "Leu added by cloning strategy"
                                                                                                                                                                          Location/Qualifiers
                                                  D9D10 heavy chain fusion protein.
                               12-AUG-1999 (first entry)
                                                                                                                                                                                                                                          138..467
                                                                                                                                                                                                                                                               Misc-difference 468
                                                                                                                                       Synthetic.
Mus musculus.
                                                                                                                                                                                                                                                                                                WO9909055-A2
                                                                                                                                                                                  Peptide
                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                           Domain
                                                                                                                                                                           Key
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interferon gamma; IFN; treatment; prevention; septic shock; cachexia; immune disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal

antibody; diabody; scFv; multivalent; ruminant.

Synthetic

Peptide Domain

Antibody; humanised; variable region; heavy chain; light chain;

12-AUG-1999 (first entry)

MoTAbII fusion protein.

/note= "Humanised heavy chain variable domain of D9D10"

/label= Mouse_D9D10_light_chain_signal_peptide

Location/Qualifiers

'note= "Human IgGl heavy chain constant domain"

138..467

Domain

Misc-difference

/note= "Leu added by cloning strategy"

/label= Humanised)_D9D10_ScFv

WO9909055-A2

/label= Gly(3)Ser_linker 473..711

469..472

Region Domain

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gamma) can be used as a medicant, for preventing or treating septic shock, cachexia, immune diseases including multiple sclerosis and Crohn's disease and skin disorders including bullous, inflammatory and neoplastic dermatoses. The antibody is selected from a single chain antibody (scFv), a chimeric antibody or diabody comprising the humanised variable domain of the monoclonal mouse anti-IFN gamma antibody 19910; a multivalent antibody or a ruminant antibody. The antibodies are also useful for determining IFN gamma levels in a sample. Two fusion CDNA genes encoding heavy and light chain fusion proteins of the humanised D9D10 antibody were constructed. The light chain comprised cond human human immunoglobulin kappa light chain constant region. The heavy chain immunoglobulin kappa light chain constant region. The heavy chain
                                                                                                                                          New engineered antibodies which bind and neutralise interferon-gamma - useful for prevention and treatment of septic shock, cachexia,
                                                                                                                                                                                                             New antibodies which bind and neutralise interferon-gamma (IFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 576; DB 20;
Pred. No. 4.4e-52;
                                                                                                                                                                   immune diseases and skin disorders
                                                                                                                                                                                          Disclosure, Fig 9; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.5%;
98.2%;
 98WO-EP05165
                       98EP-0870139
                                   97EP-0870122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 108; Conservative
                                                          (INNO-) INNOGENETICS NV.
                                                                                                      WPI; 1999-180969/15.
                                                                                Sablon E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                    N-PSDB; AAX08631.
14-AUG-1998;
                       18-JUN-1998;
                                   18-AUG-1997;
                                                                                 Buyse M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
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98.5%;
98.2%;
                              gamma levels in a sample.
                                                                                                                        Matches 108; Conservative
                                                                                              Query Match
Best Local Similarity
                                                      711 AA;
                                                         Sequence
                                                                                                                                                   δλ
  ö
                                        Gaps
                             09
                          1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
  ö
                                                                                            61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
  1; Indels
1; Mismatches
                                                                                                                                                                        AAW85692 standard; Protein; 711 AA.
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AAW85692 ID AAW8

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma) can be used as a medicant, for preventing or treating septic shock, cachexta, immune diseases including multiple sclerosis and Crohn's disease and skin disorders including bullous, inflammatory and neoplastic dermatoses. The antibody is selected from a single chain antibody (scFv), a chimeric antibody or diabody comprising the humanised variable domain of the mnonclonal mouse anti-TFN gamma antibody 9910; a multivalent antibody; or a ruminant antibody. The antibodies are also useful for determining IFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New engineered antibodies which bind and neutralise interferon-gamma - useful for prevention and treatment of septic shock, cachexia, immune diseases and skin disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies which bind and neutralise interferon-gamma (IFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 576; DB 20;
Pred. No. 7.4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 20; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              98EP-0870139.
97EP-0870122.
                                                                                                                                                                                                                                                                                                                                                                        98WO-EP05165
                                                                                                                                                                                                                                                                                                                                                                                                                              (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-180969/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sablon E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAW85692
                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                         18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                    25-FEB-1999
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Q
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AAR27680

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The sequences given in AAR41682-85 are encoded by the expression vector, pA44602. This vector contains open reading frames encoding the heavy chain variable region (VH) of the antibody 128.1, an ampicialin resistance gene and a histdine (histidinol) selection marker.

Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin enhancer and the human gammal constant region (CH). The VH region of 128.1 was isolated by polymerase chain reaction and cloned into plasmid pA4424. This was actieved by digesting the plasmid and the product with EcoRV and Nhel. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a Nhel size. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neurophrevent neurological disorders 9. Drain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 571; DB 14; Length 1:
Pred. No. 2.5e-52;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 11K; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY42621 standard; protein; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.6%;
Best Local Similarity 97.3%;
Matches 107; Conservative
                                                                                                                                                                                                                                                      92WO-US10206
                                                                                                                                                                                                                                                                                        91US-0800458
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                                                                                                                                                                                                                                                                                                                               (ALKE-) ALKERMES INC
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-196742/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ43844.
                                                                                                                                                                                                                                                                                        26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-2000
                                                                                                                                                                                                                                                    24-NOV-1992;
                                                                                                                                                                      WO9310819-A
                                                                                                                                                                                                             LO-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                 Friden PM;
                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY42621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17. The inventor's propose eliminating these allotypes by amino acid changes to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes" should be suitable for therapeutic use in all patients. See AAR27678-R27681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
              61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                  Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised antibodies having modified allotypic determinant useful for matching allotypes in therapy with decreased likelihood of causing undesirable immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                         Isoallotype; IgG1 Glm(1,2,17); anti-allotype response;
humanised Ab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 571; DB 13;
Pred. No. 2.5e-52;
1; Mismatches 2;
                                                                                                                                                                                                                                                                  Human immunoglobulin IgG1 CH2 region.
                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 4c; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Undefined ORF2 encoded by pAH4602.
                                                                                                                                                AAR27680 standard; Protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR41684 standard; Protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.6%;
Best Local Similarity 97.3%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91GB-0005245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92WO-GB00445
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LYNX-) LYNXVALE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-349162/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 AA;
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1991;
                                                                                                                                                                                                                             10-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                    WO9216562-A.
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Clark MR;

Seguence

AAR41684;

AAR41684 ID AAR4 XX AC AAR4 XX DT 20-C XX DE Unde

61

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Gaps

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Length 110;

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inteleukin-7.
                                  Homo sapiens.
                                                                  WO9530015-A2
                                                                                                                                  28-APR-1995;
                                                                                                                                                                   28-APR-1994;
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                                                                                                   09-NOV-1995
                                                                                                                                                                                                                                                                      Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR97264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides immunoglobulin E (IgE) antagonists comprising one or more of the FcepsilonRI receptor-binding determinant sites of human template antagonists include IgE variants comprising an immunoglobulin template and binding determinant sequences (bds) CDbds, EFbds and the sequence shown in AAY42581. The CDbds (CD loop binding determinant the EFbds (EF loop binding determinant asquence) are selected from the sequences shown in AAY42577 and sequences shown in AAY42578-Y42580. The variants are useful in raising and screening anti-IgE antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment and prophylaxis of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BZLF?, epstein-barr virus; EBV; C-type lectin; beta chain; MHC; antigen; majoř histocompatibility complex; immunoglobulin; cytotoxic T cell; autoimmune disease; myasthenia gravis; multiple sclerosis; allergy; systemic lupus erythematosus; organ transplant rejection; asthma; IL-7; tissue transplant rejection; therapy; cancer; viral disease; mouse;
                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IGE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktk 65
                               Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
receptor-binding; binding determinant sequence; anti-IgE antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 571; DB 20;
Pred. No. 2.7e-52;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Column 61-62; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR87023 standard; protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin G1 Fc region.
                                                                                                                                                                                                    94US-0232539
                                                                                                                                                                                                                                   91US-0744768
                                                                                                                                                                                                                                                     9405-0178583
Human IgG1 Fcgamma2 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 97.3
nes 107; Conservative
                                                                                                                                                                                                                                                                                                                     Jardieu PM, Presta LG;
                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-579941/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 AA;
                                                                allergic disease
                                                                                                   Homo sapiens.
                                                                                                                                                                                                  21-APR-1994;
                                                                                                                                                                                                                                   4-AUG-1991;
                                                                                                                                                                                                                                                     07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1996
                                                                                                                                  JS5965709-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases
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This sequence represents the human immunoglobulin GI Fc region, and was used in creating a BZLF2-immunoglobulin Fc fusion protein (BZLFZ/FC).

BZLF2 is a Bpstein-Barr virus (BBV) protein. To create BZLFZ/FC, this sequence, the leader sequence of mouse interleukin-7 (IL-7) (see ARR87021), a Flag octapeptide (see ARR87022) and a flexible linker (see ARR87021), a Flag octapeptide (see ARR87022) and a flexible linker (see ARR87021). The BZLFZ/FC fusion protein containing this sequence (see ARR87020). The BZLFZ/FC fusion protein members of the C-type lectin family. The C-type lectin domain is found in type II membrane proteins. The BZLFZ protein is capable of binding the beta chain of a major histocompatibility complex (MHC) class II antipen. Fusion proteins with an oligomerishing zipper domain (OZD), instead of an immunoglobulin Fc region, can also be created. BZLFZ proteins inhibit antigen-specific antibody formation, proliferation of Exhibit superantigen-like activity. The proteins can be used for treating or preventing autoimmune diseases such as myasthenia gravis, multiple sclerosis and systemic lupus erythematosus. Also, for treating or preventing autoimmune diseases such as myasthenia gravis, also, and such and such and viral and systemic lupus erythematogus. Also, for treating or preventing autoimmune diseases and viral and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epstein-Barr virus BZLF2 fusion proteins - used for treating e.g. auto-immune disease, transplant rejection, allergy, asthma, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                               Farrah TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 212;
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                                                                                                                                                                                                                                                                                                       Comeau MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 571; DB 16;
Pred. No. 5.6e-52;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                   Cohen JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 38-39; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, especially EBV infection.
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                                                                                                                                                                                                                                                                                                                                      Hutt-fletcher LM, Spriggs MK;
                                                                                                                                                                                    (UMOR ) UNIV MISSOURI.
(USSH ) US NAT INST OF HEALTH.
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Best Local Similarity 97.3%;
Matches 107; Conservative
95WO-US05348.
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                                                                                                                                                                                                                                                                                                       Armitage RJ,
                                                                                                                                                 IMMV ) IMMUNEX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or viral infection.
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us-09-674-857-8.rag

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The human IgG1 Fc region (AAW02305) can be used as a fusion partner for interleukin-17 receptor (IL-17R) proteins (see also AAW04184-85), allowing purification of recombinant IL-17R using protein A or protein G affinity chromatcography. Fusions between Fc and HY813 (see also AAW02387), a viral homologue of IL-17, and between Fc and murine CILA8 (AAW02386) were used to identify cells that were used as a source of murine IL-17R. Selected murine thymoma EL4 cells were used as a source of murine IL-17R cDNA (AAT33800).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding interleukin-17 receptor - useful for regulating immune and inflammatory responses, or to suppress graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EBV; BZLF2; beta-chain; major histocompatibility complex; MHC; class II; antigen; prevention; treatment; autoimmune disease; transplant rejection; allergy; asthma; super-antigen; IgG1; Epstein-barr virus; human; immunoglobulin G1; Fc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epstein-Barr virus protein - binds to major histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 571; DB 17; Length 212;
Pred. No. 5.6e-52;
1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comeau MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cohen JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunoglobulin G1 Fc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW47354 standard; protein; 212 AA
                                                                                                                                                                                                    Example 1; Page 33; 52pp; English.
                                                                                     :2
                                                                                     Yao
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Hutt-Fletcher LM, Spriggs MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 97.6%; al Similarity 97.3%; 107; Conservative 1
   95US-0538765
95US-0410535
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                                                                                   Fanslow WC, Spriggs MK,
                                                    (IMMV) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998
   07-AUG-1995;
23-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated Herpes virus Saimiri 14 proteins - useful for treating autoimmune disorders, transplant rejection, allergy, asthma, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a human immunoglobulin GI Fc region, which can form a claimed fusion protein with the Herpesvirus saimiri (HVS) major histocompatibility complex (MHC) class II binding protein, HVS14. The fusion protein can be used to treat cancer or viral disease, as HVS14 inhibits antigen presentation, or acts as
                             HVS14; major histocompatibility complex; MHC; Class II; allergy; binding protein; inhibition; antigen presentation; superantigen; treatment; cancer; viral disease; immunoglobulin; IgG1; Fc region; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 571; DB 17;
Pred. No. 5.6e-52;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                    Yao
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                                                                                                                                                                                                                                                                                                                                    Spriggs M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
Human Ammunoglobulin G1 Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 32; 45pp; English.
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Best Local Similarity 97.3%;
Matches 107; Conservative
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94US-0351901
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                                                                                                                                                                                                                                                                                                                                    Armitage R,
                                                                                                                                                                                                                                                                                                 (IMMV ) IMMUNEX CORP.
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                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-287183/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     or viral disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         superantigen
                                                                                                                   Homo sapiens
                                                                                                                                                WO9617939-A1
                                                                                                                                                                                                                                              06-JUN-1995;
07-DEC-1994;
                                                                                                                                                                                                                 07-DEC-1995;
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                                                                                                                                                                                 13-JUN-1996
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Sequence

AAW02305;

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AAW02305

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agents for affinity purification procedures.
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                                                                                                    212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-1995;
07-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5869286-A.
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                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                               AAW92411;
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                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                         1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                       The present sequence was used in the preparation of a synthetic construct containing the Epstein-barr virus (EBV) BZLF2 protein, which is capable of binding a beta-chain of a major histocompatibility complex (MHC) class II antigen. The protein can be used to inhibit antigen-specific antibody formation, peripheral blood monouclear cell proliferation and cytocoxic T-cell responses, e.g. in the prevention or treatment of autoimmune diseases, transplant rejection, allergies or asthma,
complex class II beta chain, useful for treating, e.g. auto-immune diseases or transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BZLF2 protein; beta chain; blood mononuclear mononuclear cell; Class II major histocompatibility complex antigen; proliferation; cytotoxic T cell response; antigen specific response; asthma; autoimmune disease; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                  61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgG1 Fc protein used to make BZLF2 fusion proteins.
                                                                                                                                                                                                                                                               Score 571; DB 19;
Pred. No. 5.6e-52;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comeau MR,
                                            Example 1; Columns 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cohen JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Column 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY23637 standard; protein; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epstein-Barr virus BZLF2 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spriggs MK;
                                                                                                                                                                                                                                                                97.68;
97.38;
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97US-0936854
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                                                                                                                                                                                                                                                                                          Matches 107; Conservative
                                                                                                                                                                                          and as a super-antigen
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                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                      212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens,
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                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T cell proliferation; T cell activation; organ; graft; rejection; autoimmune disease; allergy; asthma; treatment; inflammatory disease; B cell proliferation; immunoglobulin secretion; immunogen; IgG1; Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
response. BZLF2 is useful for inhibiting antigen-specific antibody formation, the proliferation of blood monourclear mononuclear cells, and cytotoxic T cell responses. BZLF2 is also useful for inhibiting undesirable antigen specific responses, e.g. in the treatment or prevention of asthma; for preventing or treating autolmmune disease; and for preventing tissue or organ transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated interleukin-17 receptor DNA - used to develop products for treating e.g. organ or graft rejection, autoimmune disease, allergy, asthma or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-17 receptor; immunoregulator; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                    Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                Score 571; DB 20;
Pred. No. 5.6e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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95US-0410535.
95US-0538765.
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Best Local Similarity 97.3%;
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies immunoreactive with interleukin-17 receptor protein useful in interfering with receptor binding to CTLA-8, as components of diagnostic or research assays or in affinity purification of the
                                                             Gaps
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                                                                                 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                 IL-17R; CTLA-8; interleukin 17; Herpesvirus saimiri; HVS 13;
human; antibody; immune suppression.
                                        Length 212;
                                                                                                                         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                             Indels
                                                                                                                                    97.6%; Score 571; DB 20;
97.3%; Pred. No. 5.6e-52;
iive 1; Mismatches 2;
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                                                                                                                                                                                               AAY99937 standard; Protein; 212 AA
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95US-0410535.
95US-0538765.
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                                                                                                                                                                                                                                         (first entry)
                                        Query Match 97.68
Best Local Similarity 97.38
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                             Human IgG1 Fc region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-411206/35
         212 AA;
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23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri; HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic; anti-asthmatic; immunoglobulin G1; Fc region.
                                                                  Gaps
                                                                                                                        1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                       Suppressing rejection of a grafted syngeneic or allogeneic organ or tissue in a graft recipient for organ transplantation involves transfecting the organ or tissue with DNA encoding soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating or preventing diseases like allergy, asthma and
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      Length 212;
                                                                                                                                                                                                                                           61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                      Indels
Score 571; DB 21;
Pred. No. 5.6e-52;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunoglobulin G1 Fc region.
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95US-0410535.
95US-0538765.
   Query Match 97.6%;
Best Local Similarity 97.3%;
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-17R receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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97.6%; Score 571; DB 21; Length 212;

Query Match

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AAB03809 standard; Protein; 212

AAB03809

61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an immunoresponse, for treating or preventing diseases like allergy, asthma and autoimmune diseases, and for suppressing rejection of grafted
                                                                                                                                                                                                                                                                                                                                  IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri; HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic; anti-asthmatic; immunoglobulin G1; Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regulating, treating or preventing immune or inflammatory response in mammal, especially organ or graft rejection, allergy or asthma, comprises administering interleukin-17 receptors
                                                             APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                 0;
                                                                                                        61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                      Pred. No. 5.6e-52;
1; Mismatches 2;
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                                                                                                                                                                                                             AAY97250 standard; Protein; 212 AA
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97.38;
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               Conservative
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 Best Local Similarity
Matches 107; Conser
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07-AUG-1995;
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Interleukin-17 receptor; IL-17R; CTLA8; antiinflammatory; antiallergic; immunosuppressive; organ rejection; graft rejection; autoimmune disease; allergy; asthma; IgG1; immunoglobulin G1; human.

Homo sapiens.

Fc region of human immunoglobulin G1.

13-0CT-2000

AAB03809;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to an isolated and purified interleukin-17 receptor (IL-17R). A soluble IL-17 protein (CTLAB) and a herpesvirus similar (HVS13) open reading frame (homologous to CTLAB) were expressed as fusion proteins comprising an immunoglobulin Fc region, and used to screen for the expression of the IL-17R. The screening identified the novel receptor of the invention. IL-17R. The screening identified the protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic and antiallergic activities, and is an inhibitor of T cell proliferation and activation. IL-17R can be used to regulate immune functions, and is useful for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. The present sequence represents the Fc region of human immunoglobulin G1 (1961). This fragment of 1961 forms part of the IL-17 fusion protein used to identify IL-17R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-17 receptor protein useful for regulating immune functions and for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma in human \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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95US-0410535.
95US-0538765.
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Matches 107; Conservative
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23-MAR-1995;
07-AUG-1995;
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Indels

Query Match 97.6%; Score 571; DB 21; 5 Best Local Similarity 97.3%; Pred. No. 5.6e-52; Matches, 107; Conservative 1; Mismatches 2;

Length 212;

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Search completed: June 21, 2002, 08:36:09 Job time: 323 sec

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us-09-674-857-8.rspt

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Q96pq8 homo sapien
Q95m34 equus cabal
Q9d814 mus musculu
Q91z05 mus musculu
Q9rla4 mus musculu
Q9914 mus musculu
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O96bb9 homo sapien
Q96g46 homo sapien
Q96a6 homo sapien
Q96a6 homo sapien
Q96a4 qinglymosto
                                                             June 21, 2002, 08:59:32; Search time 176.89 Seconds (without alignments) 107.578 Million cell updates/sec
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                                                                                                                           1 APELLGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                          562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                   562222 seqs, 172994929 residues
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Listing first 45 summaries
                                           OM protein - protein search, using sw model
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095M34
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Gapop 10.0 , Gapext 0.5
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    sp_plant:*
    sp_rodent:*
    sp_virus:*
    sp_vertebrate:*
    sp_unclassified:*
                                                                                                                                                                                                                                                                                                                   sp_archa:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_lnvertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_organelle:*
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Maximum DB seq length: 2000000000
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                                                                                                        US-09-674-857-8
585
                                                                                                                                                                                                                                                                                                                                                                           sp_mammal:*
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Match Length
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468
473
375
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2233.6699.75
2233.6699.75
2233.6699.75
2233.6699.76
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405
405
396.5
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                                                                                                                                                                                                                                                                                                         Database :
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0948w4 mus musculu 091v32 m adult mal 09up60 homo sapien 09pk68 homo sapien 096k8 homo sapien 096k8 homo sapien 096k8 homo sapien 096k10 homo sapien 099m1 mus musculu 099k20 homo sapien 099k20 mus musculu 099k20 mus musculu 091v25 mus musculu 091v25 mus musculu 091v25 mus musculu 091v21 mus musculu 091v27 mus musculu 099v2787 drosophila	ALIGNMENTS  PRT; 701 AA.  19, Created)  19, Last sequence update)  19, Last annotation update)  10, Last annotation update)  11593034;  11 mouse models of prostatic cancer.";  12 mouse models of prostatic cancer.";  13 mouse models of prostatic cancer.";  14 mouse models of prostatic cancer.";  15 mm; 94ACGCEB42CC992F CRC64;	HED HED
09D8W4 09JV32 09JV32 09JV32 099K68 096K68 096K68 096K68 099KX8 099KX0 099KX0 099KX0 099KX0 099KX1 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73 09JW73	ALIGNMENTS  Created) Last sequence update) Last annotation updat Last annotation updat ANT IMMUNOCONJUGATE. Ta; Craniata; Vertebrat S; Catarrhini; Hominid Tumor vascular endoth mouse models of prosta A. 94.1285(2001 A. 94.265E842CC992F C W; Score 571; DB 4; L	Pred. No. 9.3 1; Mismatches IISRTPEVTCVVDVS
20.8 130 11 20.4 4 416 4 20.4 4 496 4 20.5 4 496 4 20.6 5 235 11 19.0 5 235 11 19.1 6 235 11 19.1 6 236 11 18.2 481 11 18.3 488 11 18.4 426 11 18.5 481 11 18.7 486 11 18.7 486 11 18.7 486 11 18.7 481 11 18.7 5 233 11 17.6 233 11 17.6 233 11 17.6 233 11 17.6 238 11	NARY; rel: rel: rel: rel: rel: rel: rel: rel:	111ar1ty 97.3%; Conservative GPSVFLFPPKPKDTLM H
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	RESULT 1 D D D D D D D D D D D D D D D D D D D	Be Ma Qy Db

61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 

337 AA

PRT;

PRELIMINARY;

Q95M34 N

RESULT Q95M34 ID Q9

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Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.4%; Score 400; DB 11; Length 473; llarity 66.4%; Pred. No. 5.3e-36; Conservative 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 THREDINSTIRVVSALPIQHQDWASGKEFKCKVNNKDLPSPIERTISKIK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL EMBL EMBL) = 1. BYPOThetical protein. SEQUENCE 473 Aa; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA PROTEIN.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                Query Match 69.2%; Score 405; DB 11;
Best Local Similarity 66.4%; Pred. No. 1.5e-36;
Matches 73; Conservative 18; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 AA.
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Best Local Similarity
Matches 73; Conserv
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Q91205;
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Q9R1A4;
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Ry SEQUENCE FROM N.A.

RY STAIN—C57BL/61; TISSUE=PANCREAS;

RY RAIN—C57BL/61; TISSUE=PANCREAS;

RY RAIN—C57BL/61; TISSUE=PANCREAS;

RY RAVAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa M., Mishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,

RA Lydis P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
                                                                                                                                                                                                                                                              MEDLINE-98383416; PubMed-9717671; Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.; Gorganization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-119(1998).

EMBL: AJ300675; CAC44624-1: -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 337;
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                                                                                                                                                                                                                  Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFDIF6 CRC64;
           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 80.7%; Score 472; DB 6;
1 Similarity 76.4%; Pred. No. 3.6e-44;
84; Conservative 15; Mismatches 11;
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                                                                                                          Equus caballus (Horse).
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                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID=9796;
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                                                                            (FRAGMENT).
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                                                                                                                          Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                    62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                            308 REEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 356
                                           Length
                                                                                                                      15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; EM003878; ARH03878.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Incer. | Pfant | PF00047; | 15; | 2. | SMART; SM00409; | IG; | 2. | SMART; SM00409; | IGc. | 13. | 13. | 14. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 15. | 1
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                       DB 11;
                                       Score 396.5; DB 1
Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 AA
                                                                                                                  20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Last seque 01-DEC-2001 (TrEMBLrel. 19, Last annot SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 099L25;
01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003599; Ig.
Interpro; IPR003597; Ig.Cl.
Interpro; IPR003600; Ig_Llike.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_W.
                                   67.8%;
65.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 65.58
Matches 72; Conservative
                                                                                                                  71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              099125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99L31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
Q99L31
                                                                                                                                                                                                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SO DRAPACO O SE PACO O SE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                        Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIS2372; AAD40243.1;
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 REEQFNSTERSVSELPIMHQDMLNGKEFKCRVNSAAFPAPIEKTISKTK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48142 MW; 5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.8%; Score 396.5; DB 11; 65.1%; Pred. No. 1.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seque
01-DEC-2001 (TrEMBLrel. 19, Last annot
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
SMO0410; IG_like; 1.
SEQUENCE 463 AA; 51007 MW; EAA6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003599; Ig.
Interpro; IPR003597; Ig.cl.
Interpro; IPR003500; Ig_Llke.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 65.1%
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 AA;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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NON_TER
SEQUENCE
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RESULT 099LC4

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Q9BQB8
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                                      RESULT 10
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                                                             09BQB8
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                                                                                                      ACCOONTINUE OF THE STANDARD OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 VFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                       Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.6%; Score 138; DB 4; Length 375; 28.7%; Pred. No. 4.5e-07; Live 25; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                           67.0%; Score 392; DB 11; Length 4'65.5%; Pred. No. 4.1e-35;
1ve 17; Mismatches 21; Indels
             Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1;
HSSP; P01842; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003506; Ig.like.
InterPro; IPR003506; Ig.MGC.
InterPro; IPR003506; Ig.MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-LYMPH, LYMPHOMA;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004476; AAH04476.1; -.
HSSP; P01857; IFC1.
                                                                                                                                                                                     | District | PR003597; | Ig.cl. |
| InterPro; | PR003600; | Ig_like. |
| InterPro; | IPR003000; | Ig_like. |
| InterPro; | IPR003006; | Ig_like. |
| SMART; SM00407; | Ig. 3. |
| SMART; SM00407; | Ig.like; | 1. |
| SMART; SM00407; | Ig_like; | 1. |
| Hypothetical protein. |
| SEQUENCE 375 AA; | 41314 MW; | BlA0A0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 41.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 65.5% tes 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28,7%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Si
Matches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BSZ1
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Q9BSZ1
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Gaps
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                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
HYPOTHETICAL 65.3 KDA PROTEIN.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOBI_TAXID=9606;
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Best Local Similarity 28.7%; Pred. No. 8e-07;
Matches 29; Conservative 25; Mismatches 45; Indels
                                                                                                                                                                                                                                                             Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
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TISSUE-LYMPH, LYMPHOMA;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0002963; AAH02963.1; -.
HSSP; P01825; 7FAB.
InterPro; IPR003599; Ig.
                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG_MHC, UNKNOWN_3.
: 65300 MW; 2DAFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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    PRT;
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Interpro; IPR00359; Ig.cl.
Interpro; IPR003500; Ig_like.
Interpro; IPR003506; Ig_like.
Interpro; IPR003506; Ig_like.
Interpro; IPR0040; Ig; S.
SWART; SW0040; Ig; 2.
SWART; SW00407; IGcl; 4.
SWART; SW00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOP SEQUENCE 597 AA; 65300 MW; ;
                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JAN-2001) to the EME
EMBL; BC006180; AAH06180.1; --
EMBL; BC001872; AAH01872.1; --
HSSP; P01825; 7FAB.
PRELIMINARY;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=RHABDOMYOSARCOMA;
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                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=9606;
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NCBI_TaxID #9606;
       NCBI_TaxID-9606;
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Q96AA6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNAT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN
HYPOTHETICAL 65.0 KDA PROTEIN
EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:20337).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.6%; Score 138; DB 4; Length 597; 28.7%; Pred. No. 8e-07; Live 25; Mismatches 45; Indels
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003600; Ig_like.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SNART; SN00400; IG; 2.
SNART; SN00410; IG; 1.
SNART; SN00410; IG_like; 1.
SNART; SNO0410; IG_like; 1.
SNART; SNO040; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC015760; AAH15760.1; -. Hypothetical protein. SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | :: || :| || 426 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPR 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
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Matches 29; Conservative
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Q96BB9;
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Q96EY0
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Q96BB9
       DR DR DR DR XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                        ; Score 138; DB 4; Length 613;
; Pred. No. 8.2e-07;
25; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE-PRIMARY B-CELLS FROM TONSILS; Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC009851; AAH09851.1; -. SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                            .1857.1; -.
67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:15420).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      70 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
23.6%; Score 138; DB 4;
Best Local Similarity 28.7%; Pred. No. 8.3e-07;
Matches 29; Conservative 25; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       618 AA
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                                                                                                                                                                                                           23.6%;
28.7%;
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Strausberg R.;
                                                                                                                                                                                     Query Match
Best Local Similarity 28.7%
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SEQUENCE FROM N.A.
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Search completed: June 21, 2002, 08:59:33 Job time: 1632 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model	June 21, 2002, 09:00:25 ; Search time 48.19 Seconds (without alignments) 88.382 Million cell updates/sec	US-09-674-857-8 585 1 APELLGGPSVFLFPPKPRDTCKVSNKGLPSSIEKTISKAK 110	BLOSUM62 Gapop 10.0 , Gapext 0.5
OM protein - prot	Run on:	Title: Perfect score: Sequence:	Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	homod	уошо	P01860 homo sapien	рошо	rattn	P01870 oryctolagus		P22436 mus musculu	P03987 mus musculu	mus	P01863 mus musculu	P01865 mus musculu	P20762 rattus norv	P01866 mus musculu	mns	P01868 mus musculu	P01869 mus musculu	P20759 rattus norv	P20760 rattus norv	P01854 homo sapien						homo	homo	mesoc	mns	mus mu	3 gallu	74 canis	P01843 mus musculu
SUMMARIES	;	QT	GC1_HUMAN	GC4_HUMAN	GC3_HUMAN	GC2_HUMAN	GCB_RAT	GC_RABIT	GC2_CAVPO	GC3_MOUSE	GC3M_MOUSE	GCAB_MOUSE	GCAA_MOUSE	GCAM_MOUSE	GCC_RAT	GCB_MOUSE	GCBM_MOUSE	GC1_MOUSE	GC1M_MOUSE	GC1_RAT	GCA_RAT	EPC_HUMAN	EPC_RAT	MUC_SUNMU	EPC_MOUSE	MUC_HUMAN	ALC_RABIT	MUCB_HUMAN	KAC_HUMAN	MUC_MESAU	MUC_MOUSE	MUCM_MOUSE	LAC_CHICK	MUC_CANFA	LAC1_MOUSE
		90	Н	Н	Н	Н	Н	-	٦	Н		-+	Н	-	Н	H	-	Н	Н	~	-	<del>, -</del>	-	-	Н	Н	Н	Н	_	٦	Н	7	П	_	-
	1	Match Length	330	327	290	326	333	323	329	329	398	335	330	399	329	336	405	324	393	326	322	428	429	457	421	454	299	391	106	454	455	476	103	450	105
ф	Query	Match	97.6	9.96	91.1	90.4	76.1	٠.		71.6	71.6	69.2	68.5	68.5	68.4	68.4	68.4	67.8		65.0	57.9	28.5	26.2	26.2	23.6	23.6	23.5	23.5	22.6	22.1	22.1	22.1	21.7		20.8
	Č	score	571	265	533	529	445	435	432	419	419	405	401	401	400	400	400	396.5	396.5	380	339	166.5	153	153	138	138	137.5	136	132	129	129	129	127	_	121.5
	Result	2	1	2	Э	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

	P04221 oryctolagus P01877 homo sapien				
LAC5_MUSSP MUC_RABIT	MUCM_RABIT ALC2_HUMAN	ALC1_HUMAN LAC5_MOUSE	ALC_MOUSE HVC3_HETFR	ILL1_HUMAN	HVC1_HETFR
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105 458	340	353 105	344	213	370
20.8	20.5	20.4	19.1	18.9	18.7
121.5	119.5	119.5	111.5	110.5	109.5
34 35	37	0 0 4 0 0 0	417	44	45

## ALIGNMENTS

RESULT 1 GC1_HUMAN ID GC1_HUMAN STANDARD; PRT; 330 AA. AC P01857;			RN [1] RP SEQUENCE FROM N.A. ' SEQUENCE FROM N.A. ' RX MEDLINE-82274238; PubMed-6287432; RA Ellison J.W., Berson B.J., Hood L.E.; RT "The nucleotide sequence of a human immunoglobulin C gammal gene."; RI Nucleic Acids Res. 10:4071-4079(1982).				RN 12)  RN 12DUBUCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  RX MEDLINE-83289131; PubMed-6884994;  RA Schmidt W.E., Jung HD., Palm W., Hilschmann N.;  RT "Three-dimensional structure determination of antibodies. Primary  RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  RN [6]  RN MEDLINE-71064027; PubMed-4923144;
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GC4_HUMAN
P01861;
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                                                                                                                                                 "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9 - and 2.96.A resolution.";

Biochemistry 20:2361-2370(1981).

-I- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.

-I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35.116,198,269 & 272.

-I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 155.166,177,195,198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
                                     Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
1961 immunoquobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
[8]
                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_c1.
InterPro; IPR003509; Ig_like.
Pfam; PF00047; Ig] 3.
SMART; SW00410; IG_like; 1.
SMART; SW00407; IG_like; 1.
IMMINOGLOBULIN domain; Immunoglobulin C'region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D -> E (IN GIM(NON-1) MARKER).
/FIIGUVAR_003887.
L -> M (IN GIM(NON-1) MARKER).
/FIIGUVAR_003888.
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INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
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/FT1d=VAR_003886.
D -> F / F
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                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; PubMed=7236608;
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HINGE.
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00228; AAC82527.1; ALT_INIT.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                  RESIDUES 198,267&272.
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330
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112
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134
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                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02146; GHHU.
PDB; 1FC1; 15-JUL-92.
PDB; 1FC2; 15-JUL-92.
MIM; 147100; -.
                               DISULFIDE BONDS
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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.6%; Score 571; DB 1; L 97.3%; Pred. No. 3.1e-50; ive 1; Mismatches 2;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1GGHG4.
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Best Local Similarity 97.3
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
Prinary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=77118561; PubMed=402363;
MEDLINE=77118561; PubMed=402363;
MIChaelsen T.E., Franglone B., Franklin E.C.;
"Primary structure of the 'hinge' region of human igG3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
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0
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HINGE.
CH2.
CH3.
INTERCHAIN (WITH A LIGHT CHAIN).
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1g gamma-3 chain C region (Heavy chain disease protein) (HDC)
                                                                                                                                                                                                                                                                                                          INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 96.6%; Score 565; DB 1; Length 327; Best Local Similarity 96.4%; Pred. No. 1.2e-49; Matches 106; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                         MW; 3EDBD811EF208E7A CRC64;
                                                                                                                                                                                                              Immunoglobulin domain; Immunoglobulin C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 AA
                                                                                 EMBL; K01316; AAB59394.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=81021548; PubMed=6774747;
                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_llke.
Pfam; PP00047; ig; 3.
SMART; SM00410; IG_llke; 1.
SMART; SM00407; IG_llke; 1.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE (DISEASE PROTEIN WIS)
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106
109
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HSSP; P01842; 7FAB.
MIM; 147130; -.
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P01860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REF. 2.

-I MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALLO FO THE CHI REGION.

-I MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.

-I MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.

-I MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE DISEASE TO THE SESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.

DOMAIN 12 73 HINGE.

DOMAIN 74 183 CH2.

CH2.

CH2.
                                                                                                                                                                                                                                                                                                                                                                                                       gene deletion model.';
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.
-1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LIKED (GECNAC. . . ).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
                                                                                                                                                                                                                                                                                  MEDLINE-82247835; PubMed-6808505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                     MEDLINE=77021516; PubMed=823945; Wolfenstein-Todel C., Franchone B., Prelli F., Franklin E.C.; Wholfenstein-Todel C., Franchone B., Prelli F., Franklin E.C.; The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoqiobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
[3] REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00231; AAA52805.1; ALT_SEQ.
PIR; AO2149; G3HUWI.
HSSP; PO1857; IFC1.
MIM; 147120; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR033006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
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MOD_RES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                 Ellison J.W., Hood L.E.; Linkage and sequence homology of two human immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-83001943; PubMed-6811139;
Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982).
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                                                                                                                                                              91.1%; Score 533; DB 1; Length 290; 89.1%; Pred. No. 1.8e-46;
   N-LINKED (GLCNAC. . .).
REMOVED POST-TRANSLATIONALLY.
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                                                                                                                    F -> Y (IN OMM).
/FTId=VAR_003896.
E69CBC95705B2F46 CRC64;
                QV -> EB (IN ZUC).
/FIId=VAR_003890.
P -> L (IN OMM).
/FIId=VAR_003891.
F -> Y (IN OMM).
/FIID=VAR_003892.
                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
                                                                   T -> A (IN OMM).
/FTId=VAR_003893.
S -> N (IN OMM).
/FTId=VAR_003894.
 N-LINKED (GLCNAC
                                                                                                     MISSING (IN ZUC)
/FIId=VAR_003895
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-2 chain C region.
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                                                                                                                                      290 AA; 32331 MW;
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P01859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-5925528; PubMed-7737190; Stoppini G., Garver F., Ferri G.; "Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; Biochem. J. 121:217-225(1971).
                                                                                            SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
MEDLINE-80001357; Pubmed-113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
                                                                                                                                                                                                                                                                      SEQUENCE OF 238-275 (ZIE).
MEDLINE-80114419; PubMed=118920;
Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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"The primary structure of a human 19G2 heavy chain: genetic, evolutionary, and functional implications."; J. Immunol. 125:1048-1054(1980).
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Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
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HINGE.
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Eur. J. Biochem. 228:886-893(1995)
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MEDLINE=72033500; PubMed=4940472;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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HSSP; P01857; 1FC1.
MIM; 147110; -.
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PIR; PS0018; PS0018.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                 REMOVED POST-TRANSLATIONALLY (PROBABLE)
S -> A (IN WYELOMA PROTEINS TIL & ZIE).
TyTId-VARE,003889.
C -> S (IN REF. 3).
8310878C6878CF9C CRC64;
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                      AT OR NEAR THE COMPLEMENT-BINDING SITE
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                                                                                                                                                                 Length 326;
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Pred. No. 5.1e-46;
6; Mismatches 3; Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2B chain C region.
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MEDLINE-89232738; Pubmed-3149946;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
Pfam; SM00410; IG_like; 1.
SMART; SM00407; IG_I, 2.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 91.5%;
Matches 97; Conservative
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333 AA;
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Matches 79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pratt D.M., Mole L.E.;
"Sequence studies on the constant region of the Fd sections of rabbit
immunoglobulin G of different allotype.";
Blochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                                                                                                                                                                       Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit \lg G heavy chain from the recombinant
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11 ALCELLANBOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
104 THR, AND THE E14 MARKER, 185 THR. REF.3 HAS THE D11 AND E15
MARKERS AND REF.5 THE E15 MARKER.
                                                                                                                                                                            Oryctolagus cuniculús (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
Heavy chain genes of rabbit IgG: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=70110015; PubMed=5461106;
Fuchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of
immunoglobulin G.";
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VARIANT 104 104 T -> M (IN DI1 MAR!
                                                                                                                    (Rel. 38, Last annotation update)
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MEDLINE=76135469; PubMed=1243651;
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                                                          01, Created)
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HSSP; P01857; 1FC1.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR03597; Ig_c1.
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                                                                                                                 15-JUL-1999 (Rel. 38, Las
Ig gamma chain C region.
   STANDARD;
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                                                       21-JUL-1986
21-JUL-1986
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GC_RABIT
P01870;
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MEDLINE=71058474; PubMed=4922544;
                             Biochemistry 13:4804-4811(1974).
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InterPro: JRR003006; Ig_MHC.
InterPro: JRR003597; Ig_C1.
InterPro: JRR003600; Ig_like.
Fram: PFF0047; Ig; 3.
SMART: SM00410; IG_like; 1.
SMART: SM00407; IGC1; 2.
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                                                                                                                                                                                          13 INBRED GUINEA PIGS.
PIR; A02151; G2GP.
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P22436;
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CARBOHYD
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          RTH REPARAMENT REPARAM
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2 chain C region.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
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Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
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                                                                                                                                                                                                                                                                                                                               DB 1; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.5%; Pred. No. 1.4e-36;
ive 13; Mismatches 17; Indels
V -> VPV (IN REF. 2).

Q -> E (IN REF. 3 AND 4).

M -> D (IN REF. 5).

M -> D (IN REF. 5).

O -> E (IN REF. 5).

O -> E (IN REF. 5).

E -> Q (IN REF. 5).

E -> Q (IN REF. 5).

E -> G (IN REF. 5).

E -> G (IN REF. 5).

M -> D (IN REF. 5).
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Submitted (APR-1975) to the PIR data bank
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MEDLINE=71058486; PubMed=5538616;
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                                                                                                                                                                                                                                                                35404 MW;
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Best Local Similarity 72.3%,
Conservative
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                                                                                                                                                                                                                                                             323 AA;
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P01862;
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Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin."; Biochemistry 10:26-31(1971).
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Sukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090.
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MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine 1gG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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HEAVY CHAIN).
HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-3 chain C region, secreted form.
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GCAB_MOUSE
P01864;
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TRANSMEM
DOMAIN
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SEQUENCE FROM N.A.
MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig_like; 1.
SWART; SW00410; IG_like; 1.
SWART; SW00407; IG_like; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                            Length 329;
                                                                                                                                                                                                                          Query Match 71.6%; Score 419; DB 1; Length 32 Best Local Similarity 70.1%; Pred. No. 5.9e-35; Matches 75; Conservative 15; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                64 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                            36228 MW; F45827174182BAD6 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-3 chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                             398 AA.
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Nucleic Acids Res. 11:6775-6785(1983).
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HINGE.
CH2.
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EMBĽ; J00451; -; NOT_ANNOTATED_CDS
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EEML; V01526; CAA24767.1; ALT_SEQ.
PIR; AQ2155; G3MSM.
HSSP; P01857; IFC1.
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329 AA;
                PIR; B02156; G3MSC
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P03987;
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Dognin M.J., Lauwereys M., Strosberg A.D.;
Dognin M.J., Lauwereys M., Strosberg A.D.;
Multiple amino acid substitutions between murine gamma 2a heavy chain Fc regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4011-4035[1981].
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE, FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                  InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Prono47; ig; 3.
SMART; SM00410; IGcl.
SMART; SM00407; IGcl. 2.
PROSITE; PS00290; Ig_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.6%; Score 419; DB 1; Length 398; 70.1%; Pred. No. 7.3e-35; ive 15; Mismatches 17; Indels
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
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21-JUL-1986 (Rel. 01, Last Sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2a chain C region, B allele.
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CYTOPLASMIC
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HINGE.
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Matches 75; Conservative
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1113
223
327
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InterPro; IPR003006;
InterPro; IPR003597;
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114
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398 AA;
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MEDLINE=73056887; PubMed=4565406;
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                                                                                                                                                                      EMBL; V00798; CAA24178.1; -. PIR; A02152; G2MSA.
                                                                                                                                                                                                                                        Pfam; PF00047; ig; 3. SMART; SMO0410; IG_like; 1. SMART; SMO0407; IGcl; 2.
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Best Local Similarity
Matches 73; Conserv
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Yamawaki-Kataoka Y., Miyata T., Honjo T.,
Yamawaki-Kataoka Y., Miyata T., Honjo T.,
The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.,
Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                   1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-81223894; PubMed-6787604;
Ollo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-81076554; PubMed-6777755; Sikorav J.-L., Auffray C., Rougeon F.; Stroture of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA."; Nucleic Acids Res. 8:3143-3155(1980).
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Bourgois A., Fougereau M., Rocca-Serra J.;
Determination of the primary structure of a mouse IgG2a
immunoglobulin:amino-acid sequence of the Fc fragment. Implications
for the evolution of immunoglobulin structure and function.";
Eur. J. Blochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                               Length 335;
                                                                                                                                                                       69.2%; Score 405; DB 1; Length 33' 66.4%; Pred. No. 1.5e-33; -1ve 18: Mismatches 19; Indels
                                                                                                                                       335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
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                                                                                                                 Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 19 gamma-2A chain C region, A allele.
                                                                                                                                                                                                                                                                                                                                                        330 AA.
EMBL; J00479; -; NOT_ANNOTATED_CDS.
PIR; A02153; G2MSAB.
                                                                                                                                                                                                                                                                                                                                                        PRT;
                    HSSP, P01857, IEC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; Ig; 3.
SMART; SM00410; IG_like; 1.
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                                                                                                      PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                    Local Similarity 66.49
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DISULFIDԷ BONDS.
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P01863;
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Matches
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Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
--- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPERAS TO ENCODE MEMBRANE BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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de Preval C., Fougereau M.;
"Determination of the primary structure of a mouse gamma G2
immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Biochem. 30:452-462(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.5%; Score 401; DB 1; Length 330;
llarity 66.4%; Pred. No. 3.8e-33;
Conservative 17; Mismatches 20; Indels
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, membrane-bound form.
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Immunoglobulin domain; Immunoglobulin C region.
NON_TER
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GCB_MOUSE
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                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                   MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF THE A ALLELE.
SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
4C38138BFAED3FF0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2c chain C region.
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                                                                                                                                                                                              MGD; MGI:96443; Igh.1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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Best Local Similarity 66.4%
Matches 73; Conservative
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           SEGMENT OF MU CHAINS
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HSSP; P01857; 1FC1.
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399 AA;
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"Structure of the constant and 3' untranslated regions of the murine gamma 2b heavy chain messenger RNA.";
Science 206:1299-1303(1979).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 4.8e-33;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Ig_ 3:
SMART; SM00440; IG_like; 1.
SMART; SM00407; IGcl; 2.
Immunoglobulin domain; Immunoglobulin C region.
NON_TER
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-2B chain C region.
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HINGE.
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MEDLINE-80081501; Pubmed=117548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A. (A ALLELE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.4%;
67.9%;
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249
329 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                            HSSP; P01857;
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"Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.", cell 26:19-27(1981).

1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEGMENT OF MU CHAINS.
                                                                                                                                      SEQUENCE OF 335-405 FROM N.A.
MEDLINE-8222190; PubMed=6283537;
Yamawaki-Kataoka V., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
                                                                                                                                                                                                                                SEQUENCE OF 335-378 FROM N.A.
MEDILIBE-82115295; PubMed-6799207;
ROGETS J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
                   21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2B chain C region, membrane-bound form.
                                                                                                                                                                                           immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982)
                                                                                                                NCBI_TaxID=10090;
         ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O-LINKED (GALMAC, . .).
REMOVED POST-TRANSLATIONALLY (PROBABLE).
Q -> R (IN B ALLELE).
T -> A (IN B ALLELE).
N -> D (IN B ALLELE).
M -> I (IN B ALLELE).
L -> S (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
My; 7D879662607C356E CRC64;
                                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITE THR-105.
MEDLINE-94216359; PubMed=7512967;
Mim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
Irimura T., Takahashi N., Kato K., Arata Y.;
"O-giycosylation in hinge region of mouse immunoglobulin G2b.";
J. Biol. Chem. 269:12356(1994).
-- PTW: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
MODIFIED WITH 2 STALIC ACID RESIDUES.
                                                                                                                                                   gamma
                        MEDLINE-80081502; PubMed-117549;
Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
"Sequence of the cloned gene for the constant region of murine gamma
2b immunoglobulin heavy of nain.";
Science 206:1303-1306(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
                                                                                                                                          "Mouse immunoglobulin allotypes: post-duplication divergence of 2a and gamma 2b chain genes.";
Nature 296:761-763(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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-!- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
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                                                                                                     SEQUENCE FROM N.A. (B ALLELE).
MEDLINE-82173203; PubMed=6803173;
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HSSP; P01857; 1FC1.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003597; Ig_C1.

InterPro; IPR003500; Ig_like.

Pfam; PF00047; ig; 3.

SMART; SM00410; IG_like; 1.

SMART; SM00407; IGC1; 2.

PROSITE; PS00299; IG_MHC; 1.
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[3]
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336 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO B IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [mmunoglobulin domain; Immunoglobulin C region; Transmembrane;
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CYTOPLASMIC (POTENTIAL).
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MGD: MGI:96445; Igh.3.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_c1.
InterPro: IPR003600; Ig_like.
Pfam: PP004047; ig; 33
SWART; SM00410; IG_like; 1.
SWART; SM00407; IGC1; 2.
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STANDARD;

RESULT 15 GCBM_MOUSE ID GCBM_MOUSE

Search completed: June 21, 2002, 09:00:25 Job time: 1449 sec

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Signed of gamma-1 chain C region - synthetic C Species Signed Sign
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1 APELLGGPSVFLFPPRPKDT......CKVSNKGLPSSIEKTISKAK 110
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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97.6%; Score 571; DB 4; Length 255;

IgG1

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A.Coros references: GDB:120085; OMIN:147100
A.Map position: 14032.33 -14932.33
A.Map position: 14032.33 -14932.33
A.Introns: 99/1: 114/1; 224/1
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (c.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (c.Complex: An immunoglobulin heterotetramer; immunoglobulin c.Complex: Meywords: diuplication; glycoprotein; heterotetramer; immunoglobulin homology c.MI>
F.20-85/Domain: immunoglobulin homology c.MI>
F.37-206/Domain: immunoglobulin homology c.MI>
F.37-310/Domain: immunoglobulin homology c.MI>
F.27-83.144-204,250-308/Disulfide bonds: #status experimental
F.103/Disulfide bonds: interchain (to light chain) #status experimental
F.109/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                       A Reference number: A July 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 < A'Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 < A'Rote: this sequence has the Glm(3) and Glm(non-1) markers
R:Gall, W.E.; Edelman, G.M.
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A:Tottle: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A:Tottle: A:Contents: annotation: disulfide bonds
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog enbromide cleavage products, and the disulfide bridges.
A:Contents: annotation; disulfide bonds
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R. Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
B. Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
B. Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
R. Reference number: S6939; MJD:95262687

A. Reference number: S6939; MJD:95262687

A. Status: preliminary
A. Molecule type: mRNA
A. References: EMBL:X81695

R. Khamilchi, A.A.
S. Cross references: EMBL:X81695

R. Khamilchi, A.A.
A. Reference number: S72664
A. Reference number: S72664
                       A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 *sequence_revision 19-Mar-1997 *text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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A.Molecule type: mRNA
A.Residues: 1-140, CC', 142-374 <KH2>
A.Cross-references: EMBL:X01695
C.Superfamily: immunoglobulin C region; immunoglobulin homology
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Best Local Similarity 97.3%; Pred. No. 2.2e-49;
Matches 107; Conservative 1; Mismatches 2;
                                                                 A;Reference number: A91723; MUID:83289131
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: IGHG1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174
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Accession: S13867.

Accession: S13887.

Accession: B8-113;235-330 < TAK>

Accession: B8-113;235-330 < TAK>

Accession: S13887.

Accession: S13887.

Accession: B8-113;235-330 < TAK>

Accession: B9-113;235-330 < TAK-

Accession: B9-113;236-330 < TAK-

Accession: B9-113;240 < TAK-

Accession: B9-114, Accession: B9
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A;Residueb: 1-34, 0', 36-96, K', 98-115, 0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Residueb: 1-34, 0', 36-96, K', 98-115, 0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Note: this sequence has the G1m(17) and G1m(1) markers
B; Schmidt, WEE: J Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's • Z. Physiol. Chem. 364, 713-747, 1983
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A; Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A; Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
B; Ponstingl, H: Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A; Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Cross-references: EMBL:217370
A.Kote: List sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Reconston: S36861
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C; Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C; Accession: A9343; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R; Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nicleic Acids Res. 10, 4071-4079, 1982
A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A; Reference number: A93433; MUID:82274238
                                                                                                                                             1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
              Pred. No. 1.6e-49;
1; Mismatches 2;
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A;Contents: myeloma protein Nie
A;Accession: B91668
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         97.3%;
Local Similarity 97.3
nes 107; Conservative
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A; Residues: 1-330 <ELL>
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A; Accession: A90564
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C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic, Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoslobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
                                                                                                                                       c3, c5, u) with an IGHG4 conv
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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig gamma-3 heavy chain disease proteins - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999 C;Accession: A90442; A92219; A90198; A93315; A02149 R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C. Biochemistry 19, 4304-4308, 1980
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Pred. No. 1.6e-47;
3; Mismatches 4; Indels
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A; Status: preliminary
A; More and a more and
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A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                          R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGRG3 allele (GmbO, bl,
A;Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 553; DB 2;
Pred. No. 1.6e-47;
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93.6%;
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Best Local Similarity 93.6%;
Matches 103; Conservative
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Best Local Similarity 93.6
Matches 103; Conservative
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Best Local Similarity
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A; Residues: 1-377 <HUC>
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A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap bain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C:Complex: An immunoglobulin C region; immunoglobulin homology C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C:Superfamily: immunoglobulin homology <IM1>
F:20-85/Domain: immunoglobulin homology <IM2>
F:20-85/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
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A.Residues: 1-327 <ELL>
A.Note: the Sequence was determined from the germline gene
B.Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Blochem. J. 117, 33-47, 1970
A.Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant A.Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant A.Reference number: A90249; MUID:70207560
A.Residues: 1-30;81-326 <PIN>
C.Genetics: A.Residue type: protein
A.Residue type: protein
A.Accession: A90249
A.Molecule type: protein
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104
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C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                    158 APELLGGPSVFLFPPRKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267
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                                                                                        Length 374;
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Pred. No. 8.7e-49;
                                                                                                                                                                                 Indels
                                                                                    Score 571; DB 2; L
Pred. No. 2.6e-49;
1; Mismatches 2;
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Best Local Similarity 96.4%;
Matches 106; Conservative
                                                                                    Ouery Match
Best Local Similarity 97.3%;
Matches 107; Conservative
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Best Local Similarity
40
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A; Westduces: 1-320 SELLA-
A; Kestduces: 1-320 SELLA-
A; Kestduces: 1-320 SELLA-
A; Kestduces: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A; Note: Lys-326 is probably removed posttranslationally
B; Wangd, A.C.; Tung, E.; Fudenberg, H.H.
J: Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human 1gG2 heavy chain: genetic, evolutionary, an A; Reference number: A92809; MUID:81007873
A; Reference number: A92809; MUID:81007873
A; Note: ITP:156 is at or near the complement-binding site
A; Note: ITP:156 is at or near the complement-binding site
A; Note: ITP:156 is at or near the complement-binding site
A; Note: ITP:156 is at or near the complement-binding site
A; Reference number: A90752; MUID:80001357
A; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can J. Biochem: 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of A; Reference number: A90752; MUID:80011357
A; Contents: Myeloma protein
A; Residuces: 1-24, E'.26-57, EV'.60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'O', 1
A; Residuces: 1-24, 'E'.26-57, 'EV'.60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'O', 1
A; Reference number: A93132; MUID:80114419
A; Reference number: A93132; MUID:80114419
A; Reference number: A93132
A; Molecule type: protein
A; Residuces: 218-75 CHGP>
A; Reference number: A93132
A; Rodiecule type: protein
A; Residuces: 238-275 CHGP>
A; Reference number: A93132
A; Rodiecule type: protein
A; Reference number: A93132
A; Rodiecule type: protein
A; Residuces: 238-275 CHGP>
A; Reference number: A93132
A; Rodiecule type: protein
A; Reference number: A93132
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A/Consolidation: 1403.3.33-14032.33
A/Map position: 1403.3.33-14032.33
A/Map position: 1403.3.33-14032.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin c region; immunoglobulin homology <IMI>F:20-85/Domain: immunoglobulin homology <IMI>F:133-202/Domain: immunoglobulin homology <IMI>F:233-906/Domain: immunoglobulin homology <IMI>F:233-906/Domain: immunoglobulin homology <IMI>F:233-202/Domain: immunoglobulin homology <IMI
F:233-202/Domain: immu
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A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amid
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Biochem. J. 121, 217-225, 1971
A: Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A: Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A: Contents: annotation; myeloma protein Sa, disulfide bonds
A: Contents: annotation; myeloma protein Sa, disulfide bonds
A: Frangione, B: Milstein, C.; Pink, J.R.L.
A: Frangione, B: Milstein, C.; Pink, J.R.L.
A: Title: Structural studies of immunoglobulin G.
A: Reference number: A93157; MID: 69064124
A: Contents: annotation; Sa, disulfide bonds
C: Genetics: ......
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Pred. No. 3.4e-45;
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                                                A; Molecule type: DNA
A; Residues: 1-326 <ELL>
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                                                                                                                                       A; Molecule type: protein
A; Residues: 1-289 CFRA>
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A; Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cd
A; Note: the sequence of residues 42-76 was taken from the reference that follows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Wolfensteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter Blacken. Blocher. Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Blochem. Blophys. Res. Commun. 71, 907-914, 1976
A.Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A.Reference number: A90198; MUID:77021516
A.Accession: A90198
A.Accession: A90198
A.Molecule type: protein
A.Residues: 59-125, EB', 128-226, 228-289 <WOL>
A.Note: Lib protein lacks most of the Vegion, all of the CHI region, and part of the R.Alexander. A.; Stelnmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.; Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A.Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletion A; Reference number: A93915; MUID:82247835
A.Constents: heavy chain disease protein Omm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma-2 chain C region - human (Species: Homo sapiens (man) C.pate: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000 (Species: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000 (Spacession: A93906; A92809; A90752; A93132; A02148 (Species: A93906; A92809; A90752; A93132; A02148 (Species: A93906; Lu S.A. 79, 1984-1988, 1982 (Species: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con A; Reference number: A93906; MUID:82197621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probable quadruplication
                                                                                                                                                                                                                                                                                                                                                                                      R.Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human 1gG3. Probable quadruplicatio
A;Reference number: A92219; MUID:77118561
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein
A;Accession: A92219
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Map position: 14432.33 -14432.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
E;203-270,Chomain: immunoglobulin homology <IMM-F;203-270,Chomain: immunoglobulin homology <IMM-F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Pred. No. 1.2e-45;
8; Mismatches 4; Indels
                                           A; Contents: heavy chain disease protein Wis A; Accession: A90442
A; Reference number: A90442; MUID:81021548
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89.1%;
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Best Local Similarity 89.1
Matches 98; Conservative
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A) Status: preliminary
A) Molecule type: mRNA
A) Residues: 1-470 cSAN>
A) Residues: 1-470 cSAN>
A) Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
B) Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
B) R) Symons, D.B.A.; Clarkson, C.A.; Beale, D.
MOL. Immunol. 26, 841-850, 1989
A) Fittle: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and A; Reference number: S06610; MUID:90097956
                                                                                                                                                                                            cDNA sequences
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N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06.Jan.1995 #sequence_revision 06-Jan.1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Reference number: S22080
                      ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3555-3573, 1994
A;Fille: Five putative subclasses of swine IgG identified from the cDNA sequence number: I47158; MUID:95015845
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                          A)Accession: 147162
A)Status: preliminary; translated from GB/EMBL/DDBJ
A)Molecule type: mRNA
A)A:Residues: 1-277 < KAC>
A);Residues: 1-277 < KAC>
A)Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 PELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGHDDPEVKFSWFVDDVEVNTATTKP 312
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74.3%; Pred. No. 8e-37;
.ive 12; Mismatches 16; Indels
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A;Note: the sequence was determined from the germline C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 453; DB 2; L
Pred. No. 1.1e-37;
4; Mismatches 9;
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A; Molecule type: DNA
A; Residues: 142-470 <SYM>
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Local Similarity
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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                cDNA sequences
                                                                                                                                                       Ig gamma 2b chain constant region - pig (fragment)

G.Species: Sus scrofa domestica (domestic pig)

C.Species: 11-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C.Accession: 147160

R.RacsKovics, 1. i. Sun, 1.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A.Title: Five putative subclasses of swine IgG identified from the cDNA sequence
A.Reference number: 147158; MUID:95015845

A.Reference number: 147158; MUID:95015845

A.Reference number: 147158; MUID:95015845

A.Residues: 1-328 - KAC>
A.Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126

C.Generics:
A.Gene: IgG2b

C.Superfamily: immunoglobulin C region; immunoglobulin homology

F;133-202/Domain: immunoglobulin homology <IMM>
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
C;Accession: 147159
J: Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequals. Reference number: 147158; MUID: 95015845
A;Reference number: 147159
A;Retession: 147159
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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174 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 219
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Local Similarity 78.8%; Pred. No. 4.2e-38;
Nes 82; Conservative 14; Mismatches 8;
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Matches 82; Conser
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Matches
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Search completed: June 21, 2002, 08:37:55
Job time: 429 sec
A; Molecule type: mRNA
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A; Residues: 1-333 <BRU>
R; Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A; Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibod A; Reference number: A25941; MUID:86287397
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A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>
R; Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A; Title: Heavy chain genes of rabbit 1gG; isolation of a cDNA encoding gamma heavy chain
A; Reference number: A93928; MUID:83299917
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C; Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999
C; Accession: A91749; A90290; A99246; A94416; A02161
R; Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A; Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot A; Reference number: A91749; MUID:84030930
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A; Residues: 1-323 < BERS.
A; Note: this sequence has the dl2 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
B; Pratt, D.M.; Mole, L.E.
B; Dratt, D.M.; Mole, L.E.
A; Pratt, D.M.; Mole, L.E.
A; Pratt, D.M.; Mole, L.E.
A; Fille: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A; Reference number: A90290; MUID: 76135469
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                                                                                                                                                                                                                  Tig gamma-2b chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
C;Accession: PS0018; B25941
R;Brueggemann, M.
Gene 74, 473-482, 1988
A;Fitle: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 REEQFINSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTISRTK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.1%; Score 445; DB 2; ilarity 72.5%; Pred. No. 8.4e-37; Conservative 18; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: immunoglobulin F; 20-82/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma chain C region - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 96/1; 117/1; 227/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Status: preliminary
A Molecule type: DNA
A Residues: 227-333 <BR2>
C Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: PS0018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B25941
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Amolecule type: protein
A; Residues: 129-131.155-172, 'D', 174-184, 'A',186, 'E',188-200, 'D',202-217, 'E',219-232,'
A; Residues: 129-131.155-172, 'D', 174-184, 'A',186, 'E',188-200, 'D',202-217, 'E',219-232,'
A; Note: this has the els allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin c region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-82/Domain: immunoglobulin homology < IMN>
F; 236-303/Domain: immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 132-143, E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wikse A;Accession: A94416
A; Residues: 88-103, W, 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <WAR>
A; Cross-references: GB:W16426; NID:g16511; PIDN:AAA31289.1; PID:g165112
A; Note: this sequence has the dil allotypic marker, 104-Met, and the e15 allotypic ma R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A; Title: Sequence studies of the Rd section of the heavy chain of rabbit immunoglobul A; Reference number: A90245; MUID:70110015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best Local Similarity 72.5%; Pred. No. 8.1e-36;
Matches 79; Conservative 13; Mismatches 17;
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Appl Appl

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ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
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TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY NEUROPHARMACEUTICAL OR
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/444,644 FILING DATE:
                              US-09-022-257-4
US-08-555-613A-50
US-09-131-247-6
US-09-131-247-6
US-09-138-950-33
US-09-178-869-4
US-09-178-869-2
US-09-178-869-2
US-08-178-869-2
US-08-178-869-2
US-08-459-512-43
US-08-459-512-43
US-08-469-657-43
US-08-466-465-8
PCT-US92-02050-43
                                                                                                                                                                                                                                                            US-09-180-100-11
US-08-236-311-7
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAC: (617) 861-9540
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-UUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 44, Application US/08444644
Patent No. 6015555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,480
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amino acid
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USA
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RESULT
                                                                                                              June 21, 2002, 08:32:15; Search time 77.71 Seconds (without alignments) 34.575 Million cell updates/sec
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Sequence 44,
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Sequence 81
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Sequence 5
Sequence 7
Sequence 6
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    /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
    /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
    /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
    /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
    /cgn2_6/ptodata/2/laa/PaCMS.pep:*
    /cgn2_6/ptodata/2/laa/PCTUS.COMB.pep:*
    /cgn2_6/ptodata/2/laa/PCTUS.COMB.pep:*
    /cgn2_6/ptodata/2/laa/PCTUS.COMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-761-277A-47

US-08-704-744-81

US-08-704-744-81

US-08-704-744-81

US-08-704-14-81

US-08-707-116A-8

US-08-707-116A-8

US-08-707-116A-8

US-08-707-116A-8

US-08-523-894-12

US-08-523-894-12

US-08-808-720-1

US-08-808-720-1

US-08-808-720-1

US-08-808-720-1

US-08-808-720-1

US-08-808-720-1

US-08-444-644-21

US-08-445-7378-90

US-08-444-644-21

US-08-232-5390-55
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                             231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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583
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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                                                                                                                                                                                                                           Sedneuce:
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Gaps
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                                                                                                                                                                                                                                                        Sequence 47. Application US/08761277A
Patent No. 5972334
GENERAL INFORMATION:
APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
TITLE OF INVENTION: Leukemia
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 327;
                                                                                                                                  61 PREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 583; DB 2; ilarity 100.0%; Pred. No. 5.9e-63; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/761,277A

PULING DATE: 06-DEC-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/644,664

FILLING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REDISTATION NUMBER: 38,233

REFERENCE/DOCKET NUMBER: GENITOPE-02406

TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08470299
Patent No. 5783181
GENEZL INFORMATION:
APPLICANT: Browne, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 327 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity
Matches 110; Conserv
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                                                                                                                                                                                                                                      US-08-761-277A-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Friden, Phillip M.

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                      1 APEFLGGPSVFLFPPKPKDTLMISRTPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKIK 60
                                                                                                                                                                                             1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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0
                                                                                                          Length 110;
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                                                                                                                                                                                                                                                                                61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                       61 PREEQFISTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
                                                                                                          100.0%; Score 583; DB 3;
100.0%; Pred. No. 1.3e-63;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 583; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.3e-63;
Matches 110; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26 NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ALK88-15AAA TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44, Application US/08232246A Patent No. 6329508 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wagner, Richard W. REGISTRATION NUMBER: 34,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 amino acids
                                                                                                                              Best Local Similarity 100.
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-444-644-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-232-246A-44
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                                                                                                            Query Match
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Sequence 81, Application US/08704744
Patent No. 5705154
GENERAL INFORMATION:
AAPLICANT: Dalie, Barbara
AAPLICANT: Murgolo, Nicholas
AAPLICANT: Andall, Stephen
TILE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NUMBER: NORMAN D. HAINSON
REGISTRATION NUMBER: BOER 1059-PCT-PFF/NDH
REGISTRATION NUMBER: BOER 1059-PCT-PFF/NDH
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELEFAX: (212) 688-9200
TELEFAX: (212) 688-9200
TELEFAX: (212) 688-9200
TELEFAX: (413) 688-9200
TELEFAX: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 583; DB 5;
100.0%; Pred. No. 8.9e-63;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Schering-Plough Corporation
2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-SEPT-1996
CLASSIFECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/20886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
  APPLICATION NUMBER: PCT/US96/13152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 2000 Gallc
CITY: Kenilworth
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: do:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 07033-0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US96-13152-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-704-744-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 583; DB 1; Length 382; Best Local Similarity 100.0%; Pred. No. 7.3e-63; Matches 110; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 275
                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION 1995
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 93105C3
FELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELECHONE: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FNACTH: 382 amino acids
                                     APPLICANT: Cunghaud, Culfau G.
APPLICANT: Clinkenbeard, Helen E.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSE: SmithKilne Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue
CITY: New York
CTTY: New York
COUNTRY: U.S.A.
ZIP: 10.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application PC/TUS9613152 GENERAL INFORMATION:
Murphy, Kay E.
Chapman, Conrad G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 382 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-470-299-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US96-13152-4
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Neeff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
STREET: SQUENCES: STREET: COPPESS:
STREET: ADDRESSE: BUNNS, DOANE, SWECKER & MATHIS
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                      Length 467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 PREEGENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 361
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
COMPUTER: PACENTIN RC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            100.0%; Score 583; DB 2;
100.0%; Pred. No. 9.6e-63;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 583; DB 4; Best Local Similarity 100.0%; Pred. No. 9.6e-63; Matches 110; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    012712-165
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FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/POCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08523894 Patent No. 6136310
                                                                            : 467 amino acids
amino acid
                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 110; Conservative
             INFORMATION FOR SEQ ID NO:
                                           SEQUENCE CHARACTERISTICS
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LENGTH: 467 amino acids
                                                                                                                                                           ; MOLECULE TYPE: protein US-07-916-098A-45
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                                                                                                                                    TOPOLOGY:
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US-08-523-894-8
                                                                            LENGTH:
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APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, BARCARET D.
APPLICANT D.
APPLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 583; DB 1; 100.0%; Pred. No. 9.6e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: WORD PERPECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION: 424
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10 SOUTH WACKER DRIVE
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REFRENCE/DOCKET NUMBER: 92,310-G
TELECO.AMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: >910/221-5317
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2987
TELEFAX: (908) 298-5388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45. Application US/07916098A Patent No. 5871732 GENERAL INFORMATION:
APPLICANT: CHISHOLM, PATRICIA L. APPLICANT: CHISHOLM, PATRICIA L.
                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-704-744-81
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ILLINOIS
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RESULT 11
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                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Zivin, Robert A.
APPLICANT: Zivin, Robert A.
APPLICANT: Joiliffe, Linda K.
APPLICANT: Joiliffe, Linda K.
APPLICANT: Bluestone, Jeffrey A.
TITLE OF INVENTION: Methods and Materials For Modulation
TITLE OF INVENTION: Of the Immuno-suppressive Activity and
TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDIG, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STARET: Texas
99.3%; Score 579; DB 2; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODFERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/07,116A
FILING DATE: 01-JUN 1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAMME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Texas
COUNTRY: United States of America
21P: 77210
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GENERAL INFORMATION:
APPLICANT: Browne, Michael J.
APPLICANT: Chapman, Corrad G.
APPLICANT: Chapman, Corrad G.
APPLICANT: Clinkenbeard, Helen E.
APPLICANT: Young, Peter R.
APPLICANT: Shatzman, Allan R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chapman, Conrad G.
Clinkenbeard, Helen E.
Young, Peter R.
Shatzman, Allan R.
                                                                                                                                               Sequence 4, Application US/08070116A Patent No. 5885573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: ARCD TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 414-3000
TELEFAX: (512) 474-7577
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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US-08-470-299-10
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Gaps
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APPLICANT: Newman, Roland A.
APPLICANT: Newfi, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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WEDDUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
ELLOATION NUMBER: US/08/470,299
FILLING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 576; DB 1;
Pred. No. 5.2e-62;
0; Mismatches 1.
TITLE OF INVENTION: No. 5783181el Compounds NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road, P.O. Box 1539 CITY: King of Prussia STATE: Pennsylvania COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: 9310C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5034
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08523894 Patent No. 6136310
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99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 382 amino acids
amino acid
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Best Local Similarity
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ZIP: 22314-3187
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                                                                                                                                                                                 19406
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326 amino acids
                                   Best_Local Similarity 99.1 Matches 109; Conservative
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Best Local Similarity 98.2°
Matches 108; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of Medium Type: Ploppy of Committee of Co
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US-08-808-720-1
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US-08-808-720-3
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       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hana, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-5EP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TGSKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 6.86
0; Mismatches
                     ATTORNEY/AGENT INFORMATION:
NAME: TESKID, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-885-6620
TELEPHONE: 703-885-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08523894 Patent No. 6136310 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                           TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
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99.1%;
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ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.8
Best Local Similarity 99.1
Matches 109; Conservative
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MOLECULE TYPE: protein

US-08-523-894-10
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; MOLECULE TYPE: protein
US-08-523-894-12
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-523-894-12
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Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 326;
                                              Indels
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                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08808720
Patent No. 6100387
GENERAL INFORMATION:
APPLICANT: Swanberg, Stephen
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
TITLE OF INVENTION: CHEMOKINE DOMAINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Incorporation COMPUTER: Description COMPUTER: Description Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 APPLICATION DATA: APPLICATION NUMBER: US/08/808,720 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.8%; Score 570; DB 3; Le 98.2%; Pred. No. 2.2e-61; Netenstehes 2;
  98.8%; Score 576; DB 4;
99.1%; Pred. No. 6.8e-62;
                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genetics Insititute, Inc.
STREET: 87 CambridgePark
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY FAGENT UNPORMATION:
ATTORNEY FAGENT UNPORMATION:
NAME: Sprunger, Sucanne
REGISTRATION NUMBER: P-41,323
REFERENCE/DOCKET NUMBER: G15291
TELEPAN (G17) 498-8284
TELEPAN: (G17) 498-8281
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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; Patent No. 6100387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.8%; Score 570; DB 3; Length 328; 98.2%; Pred. No. 2.3e-61; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Herrmann, Steve
APPLICANT: Herrmann, Steve
APPLICANT: Swanberg, Stephen
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
TITLE OF INVENTION: CHEMOKINE DOMAINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREE: 87 CambridgePark
CITY: Cambridge
STATE: MA
                  APPLICANT: Herrmann, Steve
APPLICANT: Swabberg, Stephen
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
TITLE OF INVENTION: CHEMOKINE DOMAINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Insititute, Inc.
STREET: 87 CambridgePark
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/808,720 FILING DATE: CLASSIFICATION: 530 ATTORNEYAGENT INFORMATION: NAME: Sprunger, Suzanne
                                                                                                                                                                                                                                                                ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDYTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sprunger, Suzanne
REGISTRATION NUMBER: P-41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08808720 Patent No. 6100387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: I:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.28
Matches 108; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                  USA
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 570; DB 3; Length 331; Pred. No. 2.3e-61; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/808,720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 21, 2002, 08:32:16 Job time: 90 sec
                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Sprunger. Suzanne
REGISTRATION NUMBER: P-41,323
REFERENCE/DOCKET NUMBER: G15291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498 6284
TELEFAX: (617) 496-5931
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.8%;
98.2%;
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.8
Best Local Similarity 98.2
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-808-720-5
                                                                                       CLASSIFICATION:
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8: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
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10: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
11: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
12: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
13: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
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16: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1996.DAT:*
17: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
19: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
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25: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
26: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                                                       June 21, 2002, 08:36:08; Search time 224.82 Seconds (without alignments) 54.346 Million cell updates/sec
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APEFLGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110
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                                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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	Description	Undefined ORF2 enc	Amino acid sequenc	Human IgG4. Homo	Human IqG4 Fc reqi	Immunoqlobulin C-q	Amino acid sequenc	Human IqG1 C-qamma	IL4.Y124D/IqG4 pro	Leptin 1-167/IgG4	Human IFN-beta and	Interferon alpha-i
	ID	AAR41717	AAB07478	AAB67205	AAB76425	AAW37346	AAW70801	AAY92190	AAR90921	AAW10534	AAY17903	AAW18579
	DB	14	21	22	22	18	20	21	17	18	20	18
	Query Match Length DB	110	218	218	218	327	329	329	382	396	432	433
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	583	583	583	583	583	583	583	583	583	583	583
	Result No.		7	М	4	ഗ	9	7	8	6	10	11

91US-0800458.

26-NOV-1991;

(ALKE-) ALKERMES INC

Friden PM;

WPI; 1993-196742/24. N-PSDB; AAQ43848.

443 18 AAW13564 444 20 AAY31672 653 18 AAW14935 664 18 AAW14931 664 18 AAW14931 667 16 AAR80617 67 16 AAR828808 68 13 AAR828808 64 21 AAR94406 98 21 AAY94406 99 15 AAW1622 47 18 AAW10232 86 21 AAR90922 86 19 AAW16220 67 18 AAW16220 67 18 AAW16220 67 18 AAW16220 67 18 AAW76220 67 18 AAW76220 68 20 AAW76220 69 22 AAB72229 60 22 AAB72229 60 22 AAB72229 60 22 AAB72229 61 12 0 AAW85689 61 12 0 AAW85689 61 12 0 AAW85689	Humanised anti-L-s Human 19G4 chain C 2A2 Human 19G4 exp Murine anti-porcin 3F4 Human 19G4 exp	Anti-human II-4 hu Human gamma-4 heav pre-5A8 humanised Human ACAM4/IgG4-F Human ACAM6/IgG4-F Human ACAM6/IgG4-F	secreted K monoclonal G9 CDR-graf 124D/IgG4 F n 1-167/IgG	Human gamma-4PE he Human gamma-4PE hea CD4 specific CDR-9 Human chemokine SD Human chemokine SD Human chemokine MI Human chemokine MI CTLA4-1GG4 fusion	CTLA4-modified Igg P-selectin ligand P-selectin ligand P-selectin ligand Humanised 323/A3 ( Humanised 323/A3 ( D9D10 heavy chain MoTADII fusion pro 2A2 (Chimeric) hum
		AAR80617 AAW14925 AAR28808 AAY94406 AAY94404 AAR91692	AAB11694 AAR67438 AAW10232 AAR90922 AAW10535	AAW14927 AAW14926 AAW16221 AAW76220 AAW76222 AAW76223	223 223 223 269 269 269
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## ALIGNMENTS

Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell. Undefined ORF2 encoded by plasmid pAH4808. AAR41717 standard; Protein; 110 AA. 92WO-US10206. (first entry) 24-NOV-1992; 10-JUN-1993 

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The sequences given in AAR41715-18 are encoded by the expression vector pAH4808. This vector represents the cloning of the human gamma isotype, gamma-4, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CHI, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector. This vector, in combination with the chimeric light chain vector. PAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods.
Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                             Disclosure; Fig 19J; 151pp; English.
                                                         disorders
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Sequence 110 AA;

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0
                             Gaps
                                               1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                              0
  Length 110;
                                                                                               61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                            0; Indels
100.0%; Score 583; DB 14; 100.0%; Pred. No. 4.5e-53;
                         0; Mismatches
            Best Local Similarity Acc. Matches 110; Conservative
 Query Match
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Amino acid sequence of native IgG Fc region humigG4. AAB07478 standard; protein; 218 AA. 20-OCT-2000 (first entry) AAB07478; AAB07478 RESULT ACC NOT SELECT TO THE SELECT T

IgG antibody; light chain; Fc region; effector function; cancer; allergy; asthma; LFA-1-mediated disorder; tumour; cancer.

Homo sapiens

WO200042072-A2.

20-JUL-2000.

14-JAN-2000; 2000WO-US00973.

99US-0116023. 15-JAN-1999;

(GETH ) GENENTECH INC.

Presta LG;

WPI; 2000-476035/41

New Fc region-containing polypeptides that have altered effector function due to one or more amino acid modifications in the Fc region, useful in the treatment of cancer and allergic conditions such as

Disclosure; Fig 22A; 132pp; English

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produce Fc region-containing polypeptides that have altered effector.

Tunction as a consequence of one or more amino acid modifications in
the Fc region relating to the variant polypeptides that have altered effector
the Fc region. The variant polypeptides that nantile antibody),
and LFA-Inmediated disorders. Where the polypeptide binds the HER2
and LFA-Inmediated disorders. Where the polypeptide binds the HER2
receptor, the disorder preferably is HER2-expressing cancer, e.g. a
benign or malignant tumour characterized by overexpression of the
HER2 receptor. Such cancers include breast cancer, squamous cell
cancer, small-cell lung cancer, non-small cell lung cancer,
gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical
cancer, ovarian cancer, pladder cancer, hepatoma, colon cancer,
colorectal cancer, endometrial carcinoma, salivary gland carcinoma,
kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid
cancer, hepatic carcinoma and various types of head and neck cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain
                      used to
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 apeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktk 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; immunoglobulin; multidimerization domain; ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a fusion protein, comprising a peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (Ib). The hybrid molecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used. For example the peptide ligand can bind ErbB2. The peptide ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 583; DB 21; Length 218; 100.0%; Pred. No. 1e-52;
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                AAB07474-78 represent native IgG Fc regions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Best Local Similarity 100.(
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                     218 AA;
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AAW37346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides represented in AAB7635 - AAB76420 and AAB76423 - AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences used in the ErbB2 binding ligands of the invention. Sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, system damage resulting from trauma, surgery, strokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat a netticular the synthetic peptide ligands may be used to treat in particular the synthetic peptide ligands may be used to treat. Albeimer's disease, parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease.
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                                                                                                                                                                                                                                                                                                                                                                                  Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional defliciency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
                                                                                                            Gaps
                                                                                                                                   1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                               may hind to and inhibit the activity associated with a particular target molecule.
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                                                                                   Length 218;
                                                                                                                                                                                      61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                           Indels
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                                                                                 Score 583; DB 2;
Pred. No. 1e-52;
                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Human IgG4 Fc region amino acid sequence.
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                                                                                                                                                                                                                                                                                AA.
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                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 110; Conservative 0
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                                            218 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dennis MS;
                                                                                                                                                                                                                                                                                                          AAB76425;
                                              Sequence
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This protein comprises an immunoglobulin (Ig) C-gamma-4 region.
The invention provides a method for the production of tumour-
specific Ig derived from a B-cell lymphoma patient. In the novel
method, expression plasmids containing the patient's VH region(s)
joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)
sequence and expression plasmids containing the patient's VL
region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2
(see AAT97191) sequence are cotransfected along with a selectable and
amplifiable marker into a cell line (e.g. BMS147.6.1.4), and
transfected cells are then subjected to selection and amplification.
The method permits the production of a multivalent vaccine which
reflects the degree of somatic variation found within the patient's
tumour. These novel multivalent vaccines provide superior vaccines
for the treatment of B-cell lymphoma.
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at least 2 different recombinant variable regions of immunoglobulin molecules derived from B cell lymphoma cells
  Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 327;
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                                                                                                                                                                                                                               61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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100.0%; Score 583; DB 22;
100.0%; Pred. No. 1e-52;
ive 0; Mismatches 0;
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Pred. No. 1.7e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin C-gamma-4 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW37346 standard; Protein; 327
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100.0%;
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96US-0644664.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW37346;
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1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the amino acid sequence of C-gamma-4. The protein is used in the course of the invention. The specification describes cytokine antagonists comprising only the extracellular domain of the specificity-determining component of the cytokine receptor and the extracellular domain of a signal-transducing component of the cytokine receptor. The cytokine is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15), gamma-interferon or transforming growth factor-beta (IGF-beta). The antagonist is capable of binding the cytokine to form a nonfunctional and can also be used in assays for identifying novel agonists and
                                   1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
       Gaps
       .;
0
                                                                                                                                                                                                                                                           gpl30; cytokine antagonist; interleukin; gamma-interferon;
granulocyte macrophage colony-stimulating factor; J peptide;
transforming growth factor-beta.
                                                                       PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                     Cytokine antagonists - comprising extracellular domains of specificity-determining and signal-transducing components of
     Indels
     ;
   Mismatches
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2..329
                                                                                                                                                         AAW70801 standard; protein; 329 AA.
                                                                                                                                                                                                                                                                                                                                                                  /note= "C-gamma-4"
                                                                                                                                                                                                                                      Amino acid sequence of C-gamma-4.
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-044669/04.
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Matches 110;
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                                                                                                                                                                                                                                                                                                                 Synthetic
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The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to software a non-functional intermediate which then binds to a second beta software intermediate which then binds to a second beta can be software so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex
                                                                                                                                                                                                                                                                                                                                          gpl30-C-gamma-1; cytokine; antagonist; CNTF; receptor; fusion protein;
cytostatic; immunomodulator; osteopathic.
61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                               /note= "Ser-Gly bridge" 3..329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= C-gamma-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Fig 12; 152pp; English.
                                                                                                                                                         AAY92190 standard; protein; 329
                                                                                                                                                                                                                                                                                               Human IgG1 C-gamma-4 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0101858.
99US-0313942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US22045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                 01-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-293165/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200018932-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                      AAY92190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stahl N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                               173
                                                                                                                                      AAY92190
                                                                                                           RESULT
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Gaps

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Indels

Length 329;

100.0%; Score 583; DB 20; ilarity 100.0%; Pred. No. 1.7e-52; Conservative 0; Mismatches 0;

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Length 382;

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Query Match
Best Local
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native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia.
                                                                                                                                  Gaps
                                                                                                                       1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A fusion protein (AAR90921) consists of a human interleukin-4 (IL-4) mutant, IL-4.X124D, in which tyrosine at position 124 is replaced by aspartic acid, fused to the hinge-CH2-CH3 region of human 1964. It is the product of a gene fusion (AAR12659) constructed in vector pDB952. The fusion protein can be expressed in host cells, e.g. HeLa, and used as a soluble IL-4 and/or IL-13 antagonist to treat conditions caused by undesirable effects of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New soluble protein antagonists of interleukin-4 and interleukin-13 - comprise IL-4 mutant fused to Ig constant domain, useful in treating e.g. allergy, autoimmune disease or chronic infection
                                                                                                                                                                                                                                                                                                              Interleukin-4; interleukin-13; antagonist; IL-4; IL-13; immunoglobulin; IgG; constant domain; allergy; autoimmune disease; chronic infection; IL4.Y124D/IgG4; fusion protein; therapy.
                                                                                                    ;
                                                                               Length 329;
                                                                                                                                                               61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy KE;
                                                                               Score 583; DB 21;
Pred. No. 1.7e-52;
                                                                                                   ó;
                                                                      100.0%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clinkenbeard HE,
                                                                                                                                                                                                                                    Z
                                                                                                                                                                                                                                  AAR90921 standard; Protein; 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 27; 35pp; English
                                                                                                                                                                                                                                                                                             IL4.Y124D/IgG4 protein fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0468297.
94GB-0015379.
                                                                                                                                                                                                                                                                          (first entry)
                                                                              Query Match 100.
Best Local Similarity 100.
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chapman CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-129404/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥,
                                                  329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT12659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shatzman AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukins.
                                                                                                                                                                                                                                                                                                                                                                           WO9604388-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-1995;
                                                                                                                                                                                                                                                                         09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Browne MJ,
                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                    Sequence
                                                                                                                                                                                                                                                      AAR90921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Gaps
                                                                                                    1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the leptin 1-167/19G4 hinge-CH2-CH3 fusion protein, which comprises residues 1-167 of human leptin linked to the hinge-CH2-CH3 region of the human immunoglobulin G4 (19G4) protein. The chimeric leptin, which has good pharmacological activity, combined with a prolonged clearance rate, can be used in the treatment or prophylaxis of obesity or associated conditions, e.g. atherosclerosis, hypertension and Type iI diabetes. It can also be used in cosmetic treatments for the improvement of body appearance, e.g. weight reduction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leptin; ob; obese; immunoglobulin G4; IgG4; hinge-CH2-CH3; fusion; chimeric; prolonged clearance rate; treatment; prophylaxis; obesity; atherosclerosis; hypertension; Type II diabetes; cosmetic; body appearance; weight reduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric leptin having prolonged clearance rate - useful for treatment, or prophylaxis of obesity or associated conditions, e.g. atherosclerosis, hypertension and type II diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 396;
                                                                                                                                                                                                                                61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "human IgG4 hinge-CH3-CH4 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clinkenbeard HE, Robinson JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "human leptin residues 1-167"
168-396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 583; DB 18;
Pred. No. 2.1e-52;
Score 583; DB 17;
Pred. No. 2e-52;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leptin 1-167/IgG4 hinge-CH2-CH3 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Pages 11-12; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  AAW10534 standard; Protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM PLC
100.0%;
100.0%;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-GB01388.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-1997 (first entry)
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chapman CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-077526/07
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT60717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9700319-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JAN-1997.
                                                    Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Browne MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW10534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a hyrid recombinant protein comprising interferon-beta (IFN-beta) and immunoglobulin (Ig) Fc fragment having interferon-beta (IFN-beta) and immunoglobulin (Ig) Fc fragment having long retention time in vasculature. The IFN-beta molecule is joined at its C-terminal end through a peptide linker to the N-terminal end of the Ig gamma 4 chain Fc fragment, where the peptide linker comprises the sequence shown in AANI791. The hybrid recombinant protein is useful in the treatment of multiple sclerosis and viral hepatitis of the liver. The recombinant protein by incorporating the gamma 4 chain has an enhanced stability within the circulation thereby allowing the protein to be used for effective systemic therapy. The gamma 4 chain unlike the gamma 1 chain avoids problems such as complement fixation and antibody-dependent cell-mediated cytotoxicity. The present sequence reference of IEN-5, the peptide linker and an
                                            Hyrid recombinant protein; interferon-beta; IFN-beta; immunoglobulin; FC fragment; peptide linker; multiple sclerosis; viral hepatitis; 19;
      Gaps
                              1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
    ;
0
                                                                                                     PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid recombinant protein comprising interferon-Beta and immunoglobulin Fc fragment
    Indels
                                                                                                                                                                                                                                                                                  Human IFN-beta and Ig Fc recombinant hybrid protein.
   ;
0
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 5-8; 7pp; English.
                                                                                                                                                                                            AAY17903 standard; Protein; 432 AA
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0994719.
95US-0579211.
96US-0719331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0994719
                                                                                                                                                                                                                                                        (first entry)
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-346986/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TANO-) TANOX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX60626
                                                                                                                                                                                                                                                                                                                                             systemic therapy
                                                                                                                                                                                                                                                      30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1997;
28-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                    US5908626-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang TW,
                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                        AAY17903;
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                                                                                                                   240
                                                                                      61
                                                                                                                                                                               AAY17903
                                                                                                                                                              RESULT
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Hybrid of interferon and immunoglobulin Fc linked via non-immunogenic peptide - is useful for treating e.g. hepatitis B or C, hairy cell leukaemia and multiple myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences, construction of an expression vector, and expression in mammalian cells. The linker is a T cell immunologically inert peptide that serves to eliminate the neo-antigenicity created by the joining of the two polypeptide moieties. It also helps to overcome steric hindrance from the Fc portion of the hybrid. The hybrid has a much longer in vivo half-life than native interferonally and will not penetrate undesired sites. It can be used to treat hepatitis B or C, hairy cell leukaemia, multiple myeloma or other cancers or viral diseases (claimed). It also serves as a model for the design and construction of other cytokine-Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human interferon-alpha (FN-alpha) joined at its C-terminal end via a claimed linker peptide (see AAW18578) to the N-terminal end of human immunoglobulin heavy chain gamma-4 Fc. It is produced by PCR amplification (see AAW69921-24) of interferon-alpha and Fc
                                                                                                                                                                                                                                      Linker peptide; fusion protein; interferon-alpha; immunoglobulin; FC; cytokine; hepatitis B; hepatitis C; hairy cell leukaemia; multiple myeloma; camcer; viral disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide sequence comprises a fusion protein composed of
                  61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                          Interferon alpha-immunoglobulin Fc fusion protein.
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                           AAW18579 standard; Protein; 433 AA.
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                                                                                                                                                                                                                                                                                                                                                                                 /label= IFB-alpha
                                                                                                                                                                                                                                                                                                                                                                                                  189..204
/label= Linker
/note= "Claim 1"
205..433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0719331.
95US-0579211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US20861
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Fc
                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-363451/33.
                                                                                                                                                                                                                                                                                                   Chimeric Homo sapie Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang TW, Yu L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT69920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-1997
                                                                                                                                            AAW18579;
                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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0;

Gaps

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100.0%; Score 583; DB 20; Length 432; 100.0%; Pred. No. 2.4e-52; Live 0; Mismatches 0; Indels 0

110; Conservative

Similarity

Query Match Local Best Loca Matches

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99WO-US03966.
                                                                                                                                                                                                                                                                                                                                                          98US-0075887.
                                                                                                                                                                                                                                                                                                                                                                            (LEXI-) LEXIGEN PHARM CORP
                                                                                                                                                  09-NOV-1999 (first entry)
                                                                                                                                                                                                      human; drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                              Gillies SD, Lan Y,
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-527594/44.
                                                                                                                                                                       Human IgG4 chain C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 AA;
                                                                                                                                                                                                                                              Key
Misc-difference
                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                              W09943713-A1
                                                                                                                                                                                                                                                                                                                                     24-FEB-1999;
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                                                                                                                                                                                                                                                                                                                 02-SEP-1999
                                                                                                                               AAY31672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                           IgG4;
                                                           287
                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised anti-L-selectin antibody HuDreg 55 comprises 2 heavy chains each having the sequence given in AAM13564 and 2 light chains each having the sequence given in AAM13563. These are encoded by the CDNA clones given in NAT61281 and AAT61280. HuDreg 55 can be used to prevent multiple organ failure associated with polytrauma and for the prevention of acute organ damage associated with extracorporeal blood circulation. The antibody inhibits interaction between the carbohydrate-recognising domain of the selectin and the corresponding cell surface receptor.
                                                                              Gaps
                                                                    1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                  ;
0
                                                                                                                                                                                                                                                               L-selectin; humanised antibody; HuDreg 55; acute organ damage; organ failure; poly-trauma; haemorrhagic-traumatic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Using anti-selectin antibody to prevent acute organ damage and multiple organ failure - during extracorporeal circulation or following polytrauma, e. g. haemorrhagic-traumatic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                             Length 433;
                                                                                                           PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                      Indels
                                                                                                                                                                                                                                            Humanised anti-L-selectin antibody HuDreg 55 heavy chain.
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100.0%; Pred. No. 2.4e-52;
tive 0; Mismatches 0;
                           100.0%; Score 583; DB 18;
100.0%; Pred. No. 2.4e-52;
tive 0; Mismatches 0;
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                                                                                                                                                                                AAW13564 standard; Protein; 443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             (BOEF ) BOEHRINGER MANNHEIM GMBH. (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                     95US-0578953.
                                                                                                                                                                                                                                                                                                                                                                   96WO-US13152
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95EP-0114696.
                                                                                                                                                                                                                         (first entry)
                            Query Match 100.
Best Local Similarity 100.
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                       Chimeric Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Co M, Haselbeck A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-165036/15.
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Best Local Similarity
Matches 110; Conserv
433 AA
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                                                                                                                                                                                                                                                                                             Chimeric Mus sp.;
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17-AUG-1995;
19-SEP-1995;
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Sednence
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1 APEPLGGSPENDERMENTALEMENTEPROVONSORDENDERMYNONCOMPHAKE 60
227 aperligapsvilppkpktilmistrperconvonysopapergrawyogvenhaktk 206
61 DAREOPRYSTRANGLOSSIEKTISAKA 110
D 287 preceptistyvssitvingdwingkepkcxsnkgipssiektiskak 336
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AAW14932 standard; Protein; 463 AA.

AAW14932

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                                                                    Heavy chain (AAW14935) and light chain (AAW14936) sequences correspond to murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody 2A2 (see also AAW14931-32). They are encoded by a 2A2 human 1g64 expression plasmid insert (see also AAT62933). A chimeric antibody specific for porcine VCAM can be produced in transfected host cells. It is useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplantation of porcine cells, tissues and organs into human
                                    Gaps
                                                    1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibodies binding to porcine but not human cell interaction proteins – useful to treat and assay for rejection of xenografted
                                  0
                                                                                                                                                                                                                                                                            2A2 Human IgG4 expression plasmid insert product (heavy chain).
        Length 444;
                                                                                                       Xenotransplantation, graft rejection; cell interaction; pig
vascular cell adhesion molecule; VCAM; monoclonal antibody;
chimeric antibody; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rollins S;
                                  Indels
Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-52;
Matches 110; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 48-50; 105pp; English.
                                                                                                                                                                                                AAW14935 standard; Protein; 463 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matis LA, Mueller EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins - useful to treat and a porcine organs, tissues or cells
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                                                                                                                                                                                                                                                                                                                                                                                  WO9711971-A1
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28-SEP-1995;
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ID AAW1
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Heavy chain (AAW14932) and light chain (AAW14931) sequences are provided for the murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (MAAD) 2A2. Hybridoma 2A2 was produced by standard techniques using recombinant, soluble porcine produced by standard techniques using recombinant, soluble porcine (VCAM as immunogen. Chimeric antibodies can be produced by cloning expression plasmid pAPRX-3P modified to contain the human gamma (constant region in place of the human gamma! Cl region Sequences are provided for 2A2 (chimeric) human G2/64 conforce (AAW14934), and 2A2 human G2/64 expression plasmid insert product (AAW14934), and 2A2 chimeric antibodies are specific for porcine VCAM. They are useful for diagnosing kuman rejection of porcine xenotransplants and for inproving xenotransplantation of porcine cells; tissues and organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies binding to porcine but not human cell interaction proteins – useful to treat and assay for rejection of xenografted porcine organs, tissues or cells
                                                                                   Xenotransplantation; graft rejection; cell interaction; pig;
vascular cell adhesion molecule; VCAM; monoclonal antibody;
chimeric antibody; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mueller JP, Rollins S;
                                                        Murine anti-porcine VCAM 2A2 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 40-42; 105pp; English.
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matis LA, Mueller EE,
                                                                                                                                                                                                                 /label= CDR2
|118..125
|/label= CDR3
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/label= CDR1
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                               (first entry)
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                              16-JUN-1997
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28-SEP-1995;
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Rother RP;
   AAW14932;
                                                                                                                                              Mus sp.
                                                                                                                                                                                       Region
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DB 18; Length 463;

100.0%; Score 583;

463 AA;

Sequence

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Indels

Score 583; DB 18; Pred. No. 2.6e-52; Mismatches 0;

100.0%; Sc 100.0%; Pr tive 0;

Best Local Similarity 100. Matches 110; Conservative

Query Match

Length 463;

1 APEFLGGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

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Query Match

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0;
                           0; Gaps
Best Locial Similarity 100.0%; Pred. No. 2.6e-52; Matches 110; Conservative 0; Mismatches 0; Indels
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op O	247 apeflggpsvflfppkpkdtlmisrtpevtcvvvdvsqedpevqfnwyvdgvevhnaktk 306

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Search completed: June 21, 2002, 08:36:08 Job time: 322 sec

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Q9up60 homo sapien
Q9up60 homo sapien
Q96k68 homo sapien
Q96kx8 homo sapien
Q96dk0 homo sapien
Q9044 pinglymosto
Q9brv0 homo sapien
Q9brg0 homo sapien
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  m adult mal
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EMBL: AF272774; AAK58686.1; ... SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
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                                                                                                                                                                                                                                                              HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.4e-52;
3; Mismatches 4; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
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Q96K68
Q96KX8
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Q91Z07
Q99KA4
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Q99LA6
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Q91WT1
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Q9DCD9
Q91XE1
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MEDLINE-21477448; PubMed-11593034;
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93.6%;
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Matches 103; Conservative
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                                                                                                                                                         June 21, 2002, 08:59:32; Search time 176.89 Seconds (without alignments) 107.578 Million cell updates/sec
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Q95m34 equus cabal
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                                                                                                                                                                                                                                                                                                   1 APEFLGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                          562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM protein - protein search, using sw model
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095M34
098LA4
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091Z05
099L31
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Q9BSZ1
Q9BU10
Q96BB9
Q96EY0
Q96GA6
Q96AA6
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_vertebrate:*
sp_unclassified:*
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sp_invertebrate:*
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sp_organelle:*
sp_phage:*
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Maximum DB seq length: 200000000
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sp_bacteria:*
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sp_rodent:*
sp_virus:*
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                      9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
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0
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                  Length 437;
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                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003435; AAH03435.1; ... HSSP; P01842; 7FAB.
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; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                            69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                             69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.5%; Score 405; DB 11; Best Local Similarity 69.6%; Pred. No. 2.5e-36; Matches 71; Conservative 18; Mismatches 13;
                69.5%; Score 405; DB 11;
69.6%; Pred. No. 2.3e-36;
ive 18; Mismatches 13;
                                                                                                                                                                                                                                                                                      463 AA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
1810060009RIK PROTEIN.
IGH-1 OR 1810060009RIK.
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InterPro; IPR00359; Ig.
InterPro; IPR00359; Ig_C1.
InterPro; IPR003509; Ig_11ke.
InterPro; IPR003506; Ig_1NC.
InterPro; IPR003506; Ig_WC.
Pfam; Pr00047; Ig; 3.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 2.
SMART; SM00401; IG_11ke; 1.
SMART; SM004010; IG_11ke; 1.
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Query Match
Best Local Similarity
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Q9D8L4
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EMBL: AJ300675; CAC44624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 APELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDSQENPDVKFNWYMDGVEVRTATTR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.0%; Score 472; DB 6; Length 337; llarity 76.4%; Pred. No. 6.9e-44; Conservative 15; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                 Wagner B.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                 Last sequence update)
Last annotation update)
CHAIN CONSTANT REGION
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-98383416; PubMed-9717671;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam; PF000047; ig; 4
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48142 MW;
              01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, IMMUNOGOBULIN GAMMA 1 HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                       Equus caballus (Horse).
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les 84; Conserv
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                                                                                                                                                                             NCBI_TaxID=9796;
                                                                                    (FRAGMENT).
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Query Match
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RP SEQUENCE, FROM N.A.

RX MEDINE-21085660; Dubmed-11217851;

RA Azawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Azawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Azawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Azawa T., Hara A., Shibata K., Xiyosawa H., Kondo S., Yamanaka I.,

RA Azawa T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,

RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,

Bakai K., Okido T., Furuco M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyosh P., Marchionni L., Mashima D.A., Kamiya M., Lee N.H.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RH Hayashizaki Y.;

RHUL, AKOO7918; BAR253491; -.

RH RMEL, AKOO7918; BAR253491; -.

RHSP: POURCHON S., FEB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.1%; Score 403; DB 11; Length 473; 65.5%; Pred. No. 4.3e-36; ive 19; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :|| ||| ||| || || || || || || || ||| ||| ||| ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001) AAH10327.1; -. Hypothetical protein. SEQUENCE 473 AA: 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN_1.
MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig_like.
InterPro; IPR003006; Ig_like.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003306; Ig_W.
Fdam; PF00047; Ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00409; IG:1; 3.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN SEQUENCE 473 AA; 51699 MW; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL 51.9 KDA PROTEIN. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91Z05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91205
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Q91205
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                                                                                                     1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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     Length 473;
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                                                                                                                                                                                                  61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :||| |||| | : ||||| | 312 THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPK 361
                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 4.

SMART; SM00409; IG; 2.

SMART; SM00400; IGv; 1.

SMART; SM00406; IGv; 1.

SMART; SM00400; IG_like; 1.

PROSITE; PRO02290; IG_MHC; UNKNOWN_1.

SEQUENCE 468 AA, 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) SIMILAR TO RIKEN CDNA 1810060009 GENE.
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01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
  Score 398; DB 11;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.9%; Score 390; DB 11; 64.5%; Pred. No. 1.1e-34;
                                                   17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; Ig.
InterPro; IPR003507; Ig_cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_WHC.
                                                   72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 64.59
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Homo sapiens (Human)
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Matches 29; Conserv
                                                                                                                                                                                                                                                                                                              HSSP; P01825; 7FAB
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   TISSUE-LYMPHOMA;
                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                              Q9BQB8
                       10
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Q9BU10
                      RESULT
Q9BQB8
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                                                                                                                                                                                                                                                                         1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL 41.3 KDA PROTEIN.
HYPOTHETICAL 41.3 KDA PROTEIN.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                            Length 473;
                                                                                                                                                                                                                                                                                                                      61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                    23.7%; Score 138; DB 4; Length 375; 28.7%; Pred. No. 5.2e-07; Live 25; Mismatches 45; Indels
                                                   InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_like.
InterPro; IPR003060; Ig_lwhc.
InterPro; IPR0047; Ig, 4.
SMART; SM00407; IGcl; 3.
SMART; SM00407; IGcl; 3.
SMART; SM00406; ICV, 1.
SMART; SM00406; IC_lke; 1.
SMART; SM00406; IC_lke; 1.
SMART; SM00406; IC_lke; 1.
SMART; SM00406; IC_lke; 1.
                                                                                                                                                                                                                                                    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-LYMPH, LYMPHOMA;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC000476; AAH04476.1;
HSSP; P01857; IFC1.
                      the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR03597; Ig_c1.
InterPro; IPR03590; Ig_like.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig_c1; 3.
SMART; SM00407; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;; Score 390; DB 11;
;; Pred. No. 1.2e-34;
18; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                          375 AA
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                           66.9%;
64.5%;
Strausberg R.; Submitted (FEB-2001) to the 'BMBL; BC003888; AAH03888.1; mn1842; 7FAB.
                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.5%
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 28.7 Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BSZ1;
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Gaps
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                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.7%; Score 138; DB 4; Length 597; 28.7%; Pred. No. 9.3e-07; ive 25; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
TISSUE-LYMPH, LYMPHOMA;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1; -.
HSSP; P01825; 7FAB.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-RHABHOOMYOSARCOMA;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC006180, AAH06180.1; -.
EMBL: BC001872; AAH01872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF0004/; 15; 2.
SMART; SM0040; 1G; 2.
SMART; SM00407; IGC.; 4.
SMART; SM00406; IGv; 1.
SMART; SM00406; IG_like; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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597 AA.
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSF; PULGAS, ......
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_like.
InterPro; IPR003006; Ig_MEC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
SWART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Conservative
PRELIMINARY;
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NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (FROTEIN FOR MGC:20337).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                          Length 597;
| InterPit | IPR003597; Ig_c1. | InterPit | IPR003600; Ig_like. | InterPro: IPR003600; Ig_like. | InterPro: IPR003506; Ig_MHC. | InterPro: IPR003596; Ig_W. | InterPro: IPR003596; Ig_V. | Pfant, PF00047; Ig; 5. | SMART; SM00400; IG; 2. | SMART; SM00400; IG; 2. | SMART; SM00410; IG_like; 1. | SMART; SM00400; IG_like; 1. | SMART; SM00410; IG_like; IG_like; 1. | SMART; SM00410; IG_like; IG_like
                                                                                                                                                                                                                                                                                                                          23.7%; Score 138; DB 4; Length 59
28.7%; Pred. No. 9.3e-07;
tive 25; Mismatches 45; Indels
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TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Best Local Similarity 28.74
Matches 29; Conservative
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Best Local Similarity 28.73
Matches 29; Conservative
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096EY0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                           23.7%; Score 138; DB 4; Length 613; 28.7%; Pred. No. 9.6e-07; Live 25; Mismatches 45; Indels
                                                           Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009851; AAH09851.1; -.
SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
11-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYOTHETICAL 67.8 KDA PROTEIN.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarhini; Hominidae
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:15420).
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SEQUENCE FROM N.A.
TISSUE=PRIMARY B-CELLS FROM TONSILS;
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SEQUENCE FROM N.A.
TISSUE-LYMPH, AND LYMPHOMA;
Strausberg R.;
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Best Local Similarity 28.78
Matches 29; Conservative
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RL Submitted (NOV-2001) to the EWBL/GenBank/DDBJ databases.

BR EMBL; BCO1356, AAH17356.1; -

KW Hypothetical protein.

SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match

Best Local Similarity 28.7%; Fred. No. 9.7e-07;

Matches 29; Conservative 25; Mismatches 45; Indels 2; Gaps 2;

QY 10 VFLFPPRFRDTLMISRTPEVTCVVVDVSQEDFEVQFNWYVDGVEVHNAKTRREEGFNST 69

DD 368 VFAIPPS-FASTLTKSTKITCLVTDLTTYD-SVTISWTRONGEAVKTHTNISESHPNAT 425

QY 70 YRVSVLTVLHQDMINGKEYRCKVSDKTGFSSTSKA 110

DD 426 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKOTISRPK 466

Search completed: June 21, 2002, 08:59:32

Job time: 1631 sec
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GC_RABIT
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## ALIGNMENTS

PRT; 327 AA. ed) sequence update) annotation update) a, Craniata; Vertebrata; Euteleostom1; a; Catarrhini; Hominidae; Homo.	gamma 4 gene."; in C.; acid sequence of th	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	in C region.	HAIN (WITH A LIGHT CHAIN). HAIN (WITH A HEAVY CHAIN). HAIN (WITH A HEAVY CHAIN).
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MEDINE-71064024; PubMed-5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
Biochemistry 9:3161-3170(1970).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.", Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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MEDLINE-71064025; PubMed-5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
                                                                                                     Length 327;
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                                                                                                   Query Match 100.0%; Score 583; DB 1; Best Local Similarity 100.0%; Pred. No. 5.8e-52; Matches 110; Conservative 0; Mismatches 0;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                          Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal igdl immunoglobulin (myeloma protein Nie). I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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L -> M (IN GIM(NON-1) MARKER).
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SNART; SN00410; IG_like; 1.
SMART; SN00410; IG_like; 1.
                  Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Michaelsen T.E., Frangione B., Franklin E.C.;
Primary structure of the 'hinge' region of human 1gG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1g gamma-3 chain C region (Heavy chain disease protein) (HDC).
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MEDLINE=84235992; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 2-326 FROM N.A.
MEDLINE-82197621; PubMed-6804948;
Ellison J.W., Hood L.E.;
"Linkage and sequence homology of two human immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Fetal liver;
MEDLINE-83001943; PubMed-6811139;
Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982).
                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                 Length 290;
 N-LINKED (GLCNAC. . .).
REMOVED POST-TRANSLATIONALLY.
                                                                                                                                                                                                                                    Score 528; DB 1; Length 29
Pred. No. 1.9e-46;
6; Mismatches 6; Indels
                                                                                                                                                                                        /FTId=VAR_003896.
E69CBC95705B2F46 CRC64;
                      / FTIG=VAR_003890.

/FTIG=VAR_003891.

/FTIG=VAR_003891.

/FTIG=VAR_003892.

/FTIG=VAR_003892.

T > A (IN OMM).

/FTIG=VAR_003893.

S > N (IN OMM).

/FTIG=VAR_003893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
                                                                                                                                                  MISSING (IN ZUC).
/FTId=VAR_003895.
F -> Y (IN OMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig gamma-2 chain C region.
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MEDLINE-81007873; PubMed-6774012;
Wang A.-C., Tung E., Fudenberg H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 99-177 AND 310-326 FROM N.A.
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                                                                                                                                                                                                                                     90.6%;
89.1%;
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Best Local Similarity 89.1%;
Local Similarity 89.1%;
Local Similarity 89.1%;
Conservative
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P01859;
CARBOHYD
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             MOD_RES
                                               VARIANT
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                                                                                                                                                                                                                                                                                                                                           Merlini G., Garver F., Ferri G.;
human anti-flavin monoclonal
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"The primary structure of a human 19G2 heavy chain: genetic, evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
[5]
SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
MEDLINE-80001357; PubMed-113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human 19G2 myeloma protein.";
can. J. Blochem. 57:758-767(1979).
                                                                                                                                                    SEQUENCE OF 238-275 (ZIE).

MEDLINE-80114419; PubMed-118920;
Hofmann T., Parr D.M.;

A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";

Mol. Immunol. 16:923-925(1979).
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PIR; A02148; G2HU.
RSSP, P01857; IFC1.
MIM: 147110; -
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR0047; Ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region.
DOMAIN 99 110 HINGE.
                                                                                                                                                                                                                                                    REVISIONS TO 25; 59; 60 AND 264-268 (ZIE). Hofmann T., Parr D.M.; Submitted (MAR-1980) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=69064124; PubMed=5782707; Frangione B., Milstein C., Pink J.R.L.; "Structural studies of immunoglobulin G."; Nature 221:145-148(1969).
                                                                                                                                                                                                                                                                                                                      MEDIINE-92255288; PubMed-7737190;
Stoppini M., Bellotti V., Negri A.,
"Characterization of the two unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CH1.
HINGE.
CH2.
                                                                                                                                                                                                                                                                                                                                                                  immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995).
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MEDLINE=72033500; PubMed=4940472;
                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-121 (DOT).
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219
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-84030930; PubMed-6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-128.
MEDLINE-76135469; PubMed=1243651;
Pratt D.M., Mole L.E.;
Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
                                                                                                                                                                           Gaps
          AT OR NEAR THE COMPLEMENT-BINDING SITE.

REMOVED FOST-TRANSLATIONALLY (PROBABLE)

S -> A (IN MYELOWA PROTEINS TIL & ZIE).

FTIId-VAR_003899.

C -> S (IN REF. 3).

8310878C6878CF9C CRC64;
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                                                                                                                                                               5 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell, Stockholm (1967).
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Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit
immined of the Fd section of the heavy chain of rabbit
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MEDLINE-81299917; PubMed=6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                               Length 326;
                                                                                                              Score 528; DB 1; Length 32
Pred. No. 2.2e-46;
4; Mismatches 4; Indels
                                                                                                                                                                                                                 65 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                             SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                          MM;
                                                                                                             Query Match 90.6%;
Best Local Similarity 92.5%;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       gamma chain C region.
                                                                                                                                                                                                                                                                                                         STANDARD;
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P01870;
DISULFID
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PIR; PSO018; PSO018.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Pred. No. 9.1e-38;
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                                                                                                                                                                                                                                                                                                                        T -> M (IN D11 MARKER).

T -> A (IN B15 MARKER).

V -> E (IN REF. 2).

Q -> E (IN REF. 3 AND 4).

O -> E (IN REF. 5).

Q -> E (IN REF. 5).

O -> E (IN REF. 5).

E -> Q (IN REF. 5).

E -> Q (IN REF. 5).

E -> Q (IN REF. 5).

N -> D (IN REF. 5).
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-JUL-1999 (Rel. 38, Last annotation update)
gamma-2B chain C region.
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Brueggemann M.;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
                                                                                                                                 EMBL; M16426; AAA31289.1; -. PIR; AO2161; GHRB. HSSP, PO1857; IFC1 InterPro; IPR0033006; Ig_MHC. InterPro; IPR003597; Ig_C1.
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SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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Rattus norvegicus (Rat)
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SEQUENCE FROM N.A.
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P20761;
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P22436;
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immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Blochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=71058471; PubMed=5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
Biochemistry 10:18-25(1971).
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MEDLINE-75036073; PubMed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary Structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                    2 PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig 19G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 gamma-2 chain C region.
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                             CHAIN).
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                                                                                          INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                       Length 333;
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76.0%; Score 443; DB 1;
Best Local Similarity 71.6%; Pred. No. 9.4e-38;
Matches 78; Conservative 19; Mismatches 12;
                                                   Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 AA
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                                                                                                                                             INTERCHAIN (INTERCHAIN (INTERCHAIN (
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MEDLINE=71058486; PubMed=5538616;
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                                                                                                                                                                                                                                36497 MW;
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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27
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1109
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253
333 AA;
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P01862;
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GC2_CAVPO
ID C21-U01
DT 21-U01
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                                                                                                                     Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=85027161; PubMed=6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine 1gG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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74.3%; Pred. No. 3.8e-37;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-3 chain C region, secreted form.
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                                                           MEDLINE=71058474; PubMed=4922544;
Biochemistry 13:4804-4811(1974).
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179 IN
105 IN
110 IN
202
178 N-
36074 MW;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 3.
SWART; SM00410; IG_like; 1.
SWART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 74.33
Matches 81; Conservative
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178
248
329 AA;
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P20762;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
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                                                                               InterPro: IPR003006; 19_MHC.
InterPro: IPR003597; 1g_c1.
InterPro: IPR003500; 1g_like.
InterPro: IPR00400; 1g_like.
Pfam: PF00047; 1g, 3.
SWART; SW00410; 1G_like; 1.
SWART; SW00407; 1Gcl; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
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MEDLINE-84041483; PubMed-6314228;
Komarcmy M., Clayton L., Rogers J., Robertson S., Kettman J.,
Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Indels
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223 CH2.
327 CH3.
36228 MW; F45827174182BAD6 CRC64;
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69.8%; Pred. No. 5.1e-35;
Live 16; Mismatches 16
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-3 chain C region, membrane-bound form.
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HINGE.
CH2.
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-; NOT_ANNOTATED_CDS
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BMBL; V01256; CAA24767.1; ALT_SEQ.
PIR; A02155; GBMSM.
HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 71.4%
Best Local Similarity 69.8%
Matches 74; Conservative
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                                                            P01857; 1FC1
                            PIR; B02156; G3MSC
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SEQUENCE
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GC3M_MOUSE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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MEDLINE-88166903; PubMed-3127222;
MEDLINE-88166903; PubMed-3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
"Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNs: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
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                                                        InterPro; IPR003600; Ig_like.
Prion, PF00047; ig; 3.
SMART; SW00407; IGClike; 1.
SMART; SW00407; IGCl; 2.
PROSTIE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.4%; Score 416; DB 1; Length 398; Best Local Similarity 69.8%; Pred. No. 6.3e-35; Matches 74; Conservative 16; Mismatches 16; Indels
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18-gamma-2C chain C region.
Rattus norvegicus (Rat).
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CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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224
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398 AA;
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RESULT 12
GCIM_MOUSE
ID GCIM_MOUSE
AC P01869;
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MEDLINE-80012837; PubMed=113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-80202559; PubMed-6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin
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J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                           CH3.
INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                  (WITH A HEAVY CHAIN) (WITH A HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36571 MW; 5FCD7B7933850773 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          69.8%; Score 407; DB 1;
68.9%; Pred. No. 4.2e-34;
iive 17; Mismatches 16;
  Immunoglobulin domain; Immunoglobulin C region.
NON_TER 1 1 1
DOMAIN 1 97 CH1.
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region.
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INTERCHAIN
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                                                           CH1.
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MEDLINE-80045036; Pubmed=115593;
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MEDLINE-78008889; PubMed=5073237;
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Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                            249
329 AA;
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Best Local Similarity
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
19 gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
Mus musculus (Anoise).
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090.
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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CHAIN).
CHAIN).
CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 324;
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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69.6%; Pred. No. 6.6e-34;
iive 18; Mismatches 13;
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HSSP: P01842; FRAB.
GlycosulteDB; P01868; MGD; MGI:96446; Igh-4.
InterPro; IPR003006; Ig_MHC.
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Best Local Similarity 69.68
Matches 71; Conservative
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324 AA;
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Query Match 69.19
Best Local Similarity 65.59
Matches 72; Conservative
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       SEQUENCE
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-80045036; PubMed=115593;

Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

Takahashi N., Mano Y.;

"Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";

Cell 18:559-568(1979).
                                                                                                    Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O., "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                   MEDLINE-8115295; PubMed-6799207;
Rogers J., Chol E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
Cell 26:19-27(1981).
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing; Transmembrane. Now_TER 1
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                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
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CH3.
                                                                                SEQUENCE OF 323-393 FROM N.A. MEDLINE-82197626; PubMed-6804950;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_C1.
Pfam: PF00047; Ig; 3.
SMART; SM00407; IGC1; 2.
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                                                                                                                                                             SEQUENCE OF 323-366 FROM N.A
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"Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of 191a and 191b allotypic forms.";

Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).

-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                             9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAIN=C57BL/6;
MEDLINE=82037861; PubMed=6170065;
Schreizer P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
"Multiple differences between the nucleic acid sequences of the IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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                                                                                                                        Length 393;
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                                                                                                                                                                                            13; Indels
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193 CYTOPLASMIC (POTENTIAL).
43386 MW; 4CC88343B7A1CE27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                           69.5%; Score 405; DB 1;
69.6%; Pred. No. 8.2e-34;
iive 18; Mismatches 13;
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15-JUL-1999 (Rel. 38, Last annotation update)
11g gamma-2A chain C region, B allele.
Mus musculus (Mouse)
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HSSP, P01857; 1RC1.
Interpro: IPR003006; Ig_MHC.
Interpro: IPR003597; Ig_C1.
Interpro: IPR003600; Ig_like.
Pfan; PF0047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
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                                                                                                                                                          Best Local Similarity 69.68
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amma 2b chain genes
in a multigenic
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-81076554; PubMed-6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bourgois A., Fougereau M., Rocca-Serra J., "Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications For the evolution of immunoglobulin structure and function."; Eur. J. Blochem. 43:423-435(1974).
  1 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de Preval C., Fougereau M.;
"Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Biochem. 30:452-462(1972).
                                                 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                              MEDLINE-81223894; PubMed-6787604;
Ollo R., Auffray C., Morchamps C., Rougeon F.;
Comparison of mouse immunoglobulin gamma 2a and gamma 2b suggests that exons can be exchanged between genes in a mu family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
19 gamma-2A chain C region, A allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=74175517; PubMed=4831970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=73056887; PubMed=4565406;
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; V00798; CAA24178.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYELOMA PROTEIN MOPC 173.
                                                                                                                                      STANDARD;
                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A02152; G2MSA
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DISULFIDE BONDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-8222190; Pubmed-6283537;
Yanawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yanawaki-Kataoka Y., Nakai S., Miyata T., Yanawa Chains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2633-2657(198).

- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SECHENT OF UT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APEFLGGPSVFLFPPKPRDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANGOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                            INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                            INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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B84361C5445A6864 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, membrane-bound form.
                                                                                                                                    PROSITE, PS00290; IG_MHC, 1.
Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.4%; Score 399; DB 1;
ilarity 65.5%; Pred. No. 2.7e-33;
Conservative 18; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, J00471; AABS9661.1; ALT_INIT.
PIR; A02184; G2MSAM.
HSSP, P01857; 1FC1.
MGD; MGI:96443; IGh-1.
                                                                                                                                                                                                                                                                                                                                                                                                           330 RI
36389 MW;
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
                               InterPro, IPR003600; Ig_like Pfam; PF00047; ig; 3. SMART; SM00410; IG_like; 1. SMART; SM00407; IGcl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Best Local Similarity
"hag 72; Conserve
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112
144
250
330
330 AA;
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DISULFID
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DISULFID
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| Interpro; IPR003006; Ig_MHC. | Interpro; IPR003597; Ig_cl. |
| Interpro; IPR003500; Ig_like. |
| Interpro; IPR00410; Ig_like. |
| Interpro; IPR00410; Ig_like; |
| Interpro; IRP00410; IG_MC. |
| Interpro; Int
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
4C38138BFAED3FF0 CRC64;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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. 0 0; Gaps Query Match 68.4%; Score 399; DB 1; Length 399; Best Local Similarity 65.5%; Pred. No. 3.4e-33; Matches 72; Conservative 18; Mismatches 20; Indels

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Search completed: June 21, 2002, 09:00:25 Job time: 1449 sec

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09:21:13 2002

Fri Jun 21

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RESULT 2
531866
C. Species: synthetic
C. Species: synthetic
C. Species: synthetic
A.Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C. Dan. 1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C. Accession: S31866
R.F. Filpula, D.
A. Description: Screeing method for protein-protein interactions of cloned gene produc
A. Reference number: S31866
A. Molecule type: mRNA
A. Residues: 1-255 <FIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
Keywords: immunoglobulin
F;1-22/Region: Bscherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 110; Conservative
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Ig gamma-1 chain C
Ig gamma-1 chain C
Ig gamma-1 chain C
Ig gamma-3 chain C
Ig gamma-3 chain C
Ig gamma-3 chain C
Ig gamma-2 chain C
Ig gamma-1 chain C
                                                                June 21, 2002, 08:37:53 ; Search time 102.05 Seconds (without alignments) 103.575 Million cell updates/sec
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gamma-2a chain
gamma-2a chain
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                                                                                                                                   1 APELLGGPSVFLFPPKPKDT......CKVSNKALPAPIEKTISKAK 110
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                 hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                            protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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S31866
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G3HUWI
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A23511
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Maximum DB seq
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Perfect
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No.
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| Ig gamma-2c chain<br>Iq qamma-2b chain | O                | 19 gamma-2a chain<br>19 gamma-2b chain | Ig gamma-1 chain C | Ig gamma-2a chain | Ig gamma-2a chain | Ig gamma-2b chain | Ig gamma heavy cha | Ig gamma-1 chain C | Ig epsilon-chain - | Ig epsilon chain C | Ig heavy chain pre | Ig epsilon chain C |
|----------------------------------------|------------------|----------------------------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S00847<br>G2MSBM                       | G2MS11<br>S06611 | S40295<br>S01321                       | PS0017             | PS0019            | B30503            | A30503            | 146732             | S14236             | I36948             | EHHO               | S04845             | EHRT               |
| 7 7                                    | 7                | ~ ~                                    | 0                  | 7                 | 7                 | ~                 | 7                  | ~                  | 7                  | 1                  | 7                  | н                  |
| 329                                    | 474              | 446                                    | 326                | 322               | 112               | 88                | 180                | 152                | 426                | 428                | 549                | 429                |
| 68<br>9.9                              | 68.9<br>68.6     | 68.4                                   | 66.4               | 60.4              | 54.4              | 46.9              | 45.1               | 30.2               | 28.2               | 28.1               | 27.5               | 27.3               |
| 404<br>404                             | 404<br>402       | 401<br>396                             | 389                | 354               | 319               | 275               | 264                | 177                | 165.5              | 164.5              | 161                | 160                |
| 30<br>31                               | 33               | 34<br>35                               | 36                 | 37                | 38                | 36                | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |
|                                        |                  |                                        |                    |                   |                   |                   |                    |                    |                    |                    |                    |                    |

## ALIGNMENTS

```
ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Dates: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Nol. Immunol. 28, 319-322, 1991
Nol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716
A;Accession: PT0207
A;Residues: 1-234 <EHRA
A;Residues: 1-234 <EHRA
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 APELLGGPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 586; DB 2;
100.0%; Pred. No. 9.3e-52;
Live 0; Mismatches 0;
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DB 4; Length 255; 100.0%; Score 586;

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Biochemistry 9, 3188-3196, 1970
A.Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A.Reference number: A90565; MUID:71064027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal IgG1 immunog
                                               A.Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A.Keference number: A91723; MUID:83289131
A.Contents: myeloma protein KOL; disulfide bonds
A.Accession: A91723
                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330
A;Note: this sequence has the Glm(3) and Glm(non-1) markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region precursor - human C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #text_change Ol-Dec-2000
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change Ol-Dec-2000
C:Accession: S69339; S72664
R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
A:Title: Structure of abnormal heavy chain-deposition disease.
A:Reference number: S69339; MUID:95262687
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1374 - KHA>
A:Cross-references: EMBL:X81695
B:Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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A; Residues: 1-140, (C',142-374 <KH2>
A; Cross-references: EMBL:X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                     A Contents: annotation; disulfide bonds
Foreker, L.; Schwarz, J.; Reichel, W.; Hischmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure enbromide cleavage products, and the disulfide bridges.
A; Reference number: A91667; MUID: 77070267
A; Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 586; DB 1;
llarity 100.0%; Pred. No. 1.4e-51;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDB:120085; OMIM:147100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Cross references: GDB:120085; ON A)Map position: 14432.33-14432.33 A;Introns: 99/1; 114/1; 224/1
                                                                                                                                                                                                                                                                             R;Gall, W.E.; Edelman, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S72664
A; Accession: S72664
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 110; Conserv
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A; Molecule type: protein
A; Residues: 1-96, 'R', 98-135 <CUN>
A; Residues: 1-96, 'R', 98-135 <CUN>
A; Note: this sequence has the Glm(3) marker, 97-Arg
B; Note: this sequence has the Glm(3) marker, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque
A; Reference number: A90564; MUID:71064025
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A; Molecule type: protein

A; Not.; 36-96, K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27

A; Note: this sequence has the Glm(17) and Glm(1) markers

B; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
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A;Residues: 136-154, °Q',156-165, °Q',167-176, °Q',178-194, `N',196-197, 'D',199-238, °E',240,
A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A.Title: Die Primaerstruktur eines monoklonalen 19G1-Immunglobulins (Myelomprotein Nie).
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                                                                    Gaps
                                                                                                                    1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                       Indels
             1e-51;
0;
                                                                Mismatches
                                  Pred. No.
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A;Contents: myeloma protein Nie
A;Accession: B91668
100.0%; PIC
                       Similarity 100.
10; Conservative
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                              Local
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A; Cross-references: GDB:119340; OMIM:147130
A; Map position: 1492.33-14932.33
A; Map position: 1492.33-14932.33
A; Introns: 997,11117, 2217,
A; Introns: 997,11117, 2217,
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85, Domain: immunoglobulin homology < IMI>
F; 99-110/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-327 < ELL>
A; Note: the sequence was determined from the germline gene
A; Note: the sequence was G.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constan A; Reference number: A90249; MUID:70207560
A; Accession: A90249
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C;Decies: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
C;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104
A;Accession: A90933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Tomain: immunoglobulin homology <IM3>
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;27-83,141-201,247-305/Disulfide bonds: interchain (to heavy chain) #status experimental
F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                        Gaps
      Gaps
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                                                            APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Pred. No. 4.8e-48;
3; Mismatches 4; Indels
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      Indels
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      Mismatches
      5,
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Best Local Similarity 93.6%;
Matches 103; Conservative
         Conservative
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A; Residues: 1-30;81-326 <PIN>
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Matches 106;
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G4HU
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R: Huck, S: Fort, P: Crawford, D.H.; Lefranc, M.P.; Lefranc, G. Nucleic Acids Res. 14, 1779-1789, 1986
A: Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A: Reference number: A35511; MUID:86148507
A: Accession: A23511
A: Molecule type: DNA
A: Residues: 1-377 <HUC>
A: Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C: Genetics: A; Gene: GDB:I19339; OMIM:147120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma-3 chain C region, form LAT - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C; Accession: A60764
R; Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A; Title: A human immunoglobulin IGHG3 allele (GmbO, bl, c3, c5, u) with an IGHG4
A; Reference number: A60764; MUID:90007613
A; Residues: preliminary
A; Residues: preliminary
A; Residues: 1-377 < HUC>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Reywords: immunoglobulin homology < IMM>
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0
                                                            Length 374;
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                                                                                                                      Indels
                                                            Score 586; DB 2;
Pred. No. 1.6e-51;
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Pred. No. 1.1e-49;
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A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglob
                                                                                                                   0; Mismatches
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20-85/Domain: immunoglobulin homology <IMM>
                                                         100.0%;
100.0%;
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96.4%;
                                                                                     Best Local Similarity 100.
Matches 110; Conservative
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Best Local Similarity
                                                            Query Match
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R; Milstein, C.; Frangione, B.
Biochem. J. 217-225, 1971
A; Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A; Reference number: A90253; MUID:72033500
A; Title: Disulphide bridges of immunoglobulin G.
A; Reference number: A9157; MUID:69064124
A; Contents: annotation; Sa, disulfide bonds
C; Genetics:
A; Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: Agonza process A, Accession: Agonza process A, Accession: Agonza process A, Accession: Agonza process A, Molecule type: protein A, Molecule type: protein A, Mote: this sequence has since been revised B, Mote: this sequence has since been revised B, Hoffmann, T.; Parr, D.M.
R. Hoffmann, T.; Parr, D.M.
A. Molecule to note on the amino acid sequence of residues 381-391 of human immunoglobuli A, Reference number: A93132; MUID:80114419
A,Contents: Zie A, Accession: A93132
A, Molecule type: protein A, Accession: A, Accession: A, A, Contents C, Molecule type: B, Molecule type: Brotein A, A, Molecule type: B, Mo
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A; Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A; Note: the revised sequence differs from that shown in having 60-Ala and in the amid
                                                                                                                                                                                                        00230; NID:932759; PIDN:CAB58438.1; PID:96066056 posttranslationally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Blochem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains a; Contents: Myelotein Zie
                                                                                                                                                                                 A.Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056 A;Note: Lys-326 is probably removed posttranslationally and A.Cross-reference is probably removed posttranslationally b. removed posttranslationally J. Immunol. 125, 1048-1054, 1980 A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, A;Fefrence number: A92809; MUID:81007873 A;Contents: myeloma protein Til
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 VAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTRPREE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
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Pred. No. 2.5e-46;
5; Mismatches 3; Indels
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92.5%;
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                                                                                     A; Molecule type: DNA
A; Residues: 1-326 <ELL>
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Best Local Similarity
Matches 98; Conserv
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Atocheselves: neavy cotain disease protein Wis

Atocheselves: neavy cotain

Atocheselves: 1-289 cFRA>

Atocheselves: 1-280 cFRA>

Atoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 12-70;72-114;116-125, E',127-133, L',135-136, E',138, Y',140-154, D',156-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: a carboxyl-terminal Lys is removed posttranslationally A:Note: this sequence may represent an allelic form or another gamma chain subclass C; Comment: The heavy chain disease protein Wis is shown.
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(Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F:203-270/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6.140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Pred. No. 8.3e-48;
7; Mismatches 2;
A; Reference number: A90442; MUID: 81021548
A; Contents: heavy chain disease protein Wis
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91.8%;
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Matches 101; Conservative
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I47162
Ig gamma 4 chain constant region - pig (fragment)
C;ppecies: Sus scrofa domestica (domestic pig)
C;pate: 21-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Racskovics, II: Sun, J: Butler, J.E.
R;Racskovics, II: Sun, J: Butler, J.E.
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Seference number: I47162
A;Accession: I47162
A;Accession: I47162
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Roleoule type: mRNA
A;Residues: 1-277 < KAC>
A;Coss-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-333 <BRU>
R; Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A; Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse
A; Reference number: A25941; MUID:86287397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig gamma-2b chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
C;Accession: PS0018; B25941
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A;Introns: 96/1; 117/1; 227/1
A;Introns: 96/1; 117/1; 227/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
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Gene 74, 473-482, 1988
Gene 74, 473-482, 1988
A;Title: Evolution of the rat immunoglobulin gamma A;Reference number: PS0017; MUID:89232738
A;Accession: PS0018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.0%; Score 463; DB 2;
79.8%; Pred. No. 3e-39;
tive 13; Mismatches
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Best Local Similarity 73.43
Matches 80; Conservative
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A:Molecule type: DNA
A:Residues: 227-333 <BR2>
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Best Local Similarity
Matches 83; Conserv
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(5) Species: Sus scrofa domestica (domestic pig)

(5) Species: Sus scrofa domestica (domestic pig)

(5) Accession: 147159

(8) Racskovics, 11, Sun, 1, Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a : A; Reference number: 147159; MUID:95015845

A; Accession: 147159

A; Accession: 147159

A; Accession: 147159

A; Accession: 147159

A; Residuary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residuas: 1-328 cKAC>

A; Conserreferences: EMBL:003779; NID:9433123; PIDN:AAA52217.1; PID:9433124
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                                                                                                                                                                                           C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Accession: 147106
B; Kacskovics, I:, Sun, J:, Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Airelie: Five putative subclasses of swine IgG identified from the cDNA sequences of A; Reference number: 147158; MUID:95015845
A; Accession: 147160
A; Reference number: 147158; MUID:95015845
A; Molecule type: mRNA
A; Residues: 1-228 CKAC>
A; Coss-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                         gamma 2b chain constant region - pig (fragment)
Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.9%; Score 46%; DB 2; Length 328
80.8%; Pred. No. 1.2e-39;
Mismatches 7; Indels
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        67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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Matches 84; Conservative 13; Mismatches
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Best Local Similarity
Matches 84; Conserv
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Query Match

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A; Molecule type: mRNA
A; Residues: 88-103, W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Residues: 88-103, W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Cross-references: GB.M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
A; Note: this sequence has the dil allotypic marker, 104-Met, and the e15 allotypic malorether, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem J. 116, 249-259, 1970
A; Title: Sequence studies of the Rd section of the heavy chain of rabbit immunoglobul A; Reference number: A90245; MUID:70110015
                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 132-143, E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wikse
A;Reference number: A94416
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75.2%; Pred. No. 7.5e-38;
tive 12; Mismatches 15
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Best Local Similarity 75.23
Matches 82; Conservative
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R.Symons, D.B.A.; Clarkson, C.A.; Beale, D.
R.Symons, D.B.A.; Clarkson, C.A.; Beale, D.
A.D.: Immunol. 126, 1898
A.Fitle: Structure of bovine immunoqlobulin constant region heavy chain gamma 1 and gamma A.Reference number: S06610; MUID:90097956
A.Accession: S06610
A.Molecule type: DNA
A.Residues: 142-470 <SYM>
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A; Residues: 1-323 <BER>
A; Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R; Pratt, D.M.; Wole, LE.
Biochem. J. 151, 337-349, 1975
A; Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A; Reference number: A90290; MUID: 76135469
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A; Molecule type: protein
A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 < PRA>
R; Residues: 1-67, 'E', 49-71, 'PV', 72-128 < PRA>
R; Martens, C. L.; Moore, K. W.; Steinmetz, M.; Hood, L.; Knight, K. L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A; Title: Heavy chain genes of rabbit 1962; isolation of a CDNA encoding gamma heavy chain
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C; Species: Orycologus cuniculus (domestic rabbit)
C; Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999
C; Accession: A91749; A90299; A90245; A94416; A02161
R; Bernstein, K.E.; Alexander, C.B.; Age, R.G.
Immunogenetics 18, 387-397, 1983
A; Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant A; Reference number: A91749; MUID: 84030930
                                                                                        Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
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A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: 91ycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;188/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Note: the sequence was determined from the germline gene
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Pred. No. 7.3e-38;
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submitted to the EMBL Data Library, November 1991
A;Reference number: $22080
A;Accession: $22080
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A;Accession: A93928
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75.2%;
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Best Local Similarity 75.23
Matches 82; Conservative
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A, Molecule type: mRNA
A, Residues: 1-470 <SAN>
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15; Indels

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SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
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/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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| Sequence 22, Appli<br>Sequence 4, Appli<br>Sequence 16, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 11, Appli<br>Sequence 11, Appli<br>Sequence 11, Appli<br>Sequence 11, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 2, Appli | Sequence 16, Appl<br>Sequence 18, Appl |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------|
| US-09-180-100-22<br>US-08-470-299-4<br>US-09-131-247-16<br>US-09-131-247-14<br>US-09-176-228-3<br>US-09-176-228-3<br>US-09-176-228-3<br>US-09-135-593-8<br>PCT-US95-03866-12<br>PCT-US95-03866-14<br>PCT-US96-10043-11<br>PCT-US96-10043-19<br>US-08-897-411-7<br>US-08-8897-411-7<br>US-08-897-411-7<br>US-08-97-336-23<br>US-08-97-336-23<br>US-08-97-356-23<br>US-08-97-356-23<br>US-08-97-356-23<br>US-08-887-352-24                                                                              | US-08-887-352B-16<br>US-08-887-352B-18 |
| 4144044555561646                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 7 7                                    |
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| 2 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 44<br>45                               |

## ALIGNMENTS

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US-0644-644-644

US-061555

GENERAL INFORMATION:
FACENCE OF INVENTION:
FILLE OF INVENTION:
FORESCENCES:
ADDRESSEE:
ADDRESS
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                            1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 586; DB 2; Length 116; Best Local Similarity 100.0%; Pred. No. 1.1e-62; Matches 110; Conservative 0; Mismatches 0; Indels
                                                                                                          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                  APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 19E Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P0718P3
                                                                                                                                                                                                                                                       Sequence 55, Application US/08232539D Patent No. 5965709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-Aug-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08430633 Patent No. 5726286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39.044
REFERENCE/DOCKET NUMBER: POTTELECOMMUNICATION INFORMATION: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 116 amino acids
Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                      Gaps
                                                                                                                                                                                        1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                              Gaps
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                                                                                                    100.0%; Score 586; DB 3; Length 110; 100.0%; Pred. No. 1e-62; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                            DB 4; Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 100.0%; Score 586; DB 4;
Best Local Similarity 100.0%; Pred. No. 1e-62;
Matches 110; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26 NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALK88-15AAA
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/08232246A Patent No. 6329508 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 110 amino acids
amino acid
                                                                                                                           Best Local Similarity 100.
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RY: USA
02173
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-444-644-21
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US-08-232-246A-21
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ADDRESSEE:
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                                                                    APPLICANT: COMEM, JEFFREY
APPLICANT: COMEN, MICHAEL
APPLICANT: COMEN, MICHAEL
APPLICANT: SPRICH, THERESA
APPLICANT: SPRICH, THERESA
TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
TITLE OF INVENTION: That Bind MHC Class II Beta Chains
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NOWBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 586; DB 1; Length 212; Best Local Similarity 100.0%; Pred. No. 2.5e-62; Matches 110; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,633
FILING DATE: 28 APR-1995
CLASSIFICATION NUMBER: 08/235,397
FILING DATE: 04/28/94
ATORNEY/AGENT INFORMATION:
NAME: PERKING, PARTICIA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2612
TELEPHONE: (206)587-0430
TELEPHONE: (206)533-0644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE CAMINO CALCA
TOPOLOGY: Innear
                                                                                                                                                                                                                                     ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATLLE
STATE: MACHINGTON
COUNTRY: USA
                              ALDERSON, MARK
ARMITAGE, RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein ORIGINAL SOURCE:
GENERAL INFORMATION:
APPLICANT: ALDERS
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CLONE: IGG1 FC
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US-08-620-694A-4
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Gaps
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APPLICANT: COMEN, MICHAEL
APPLICANT: FARRAH, THERESA
APPLICANT: FARRAH, THERESA
TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF? Proteins
TITLE OF INVENTION: That Bind MHC Class II Beta Chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                                                      MEDIUM TYPE: FLORPY disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION NATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DOALSTOON DATA:
APPLICATION: PARCH 1995
CLASSIFICATION: PARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: DOALSTOON DATA:
AND DATE: 1995
ATTORNEY/AGENT INFORMATION:
NAME: DOALSTOON DATA: DATE: 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPRONE: (206)587-0430
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNEX CORPORATION
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; Patent No. 5925734
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ALDERSON, MARK APPLICANT: ARMITAGE, RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:

ORIGINAL SOURCE:

ORIGINAL SOURCE:

ORGANISM: Human

IMMEDIATE SOURCE:

CLOME: 19G1 FC
US-08-620-694A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
           STREET: 51
                                                                                                                 USA
                                                                                STATE: WA
COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-936-854-4
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Panslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTE: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 586; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.5e-62;
Matches 110; Conservative 0; Mismatches 0;
                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
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ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: 19G1 FC
US-09-022-255-4
                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-022-696-4
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| Sequence 4, Application US/09022255 | Patent No. 6072033 |
| GENERAL INFORMATION |
| APPLICANT: Parigs, Melanie |
| APPLICANT: Fanslow, William |
| TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17 |
| NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: Immunex Corporation |
| STREET: 51 University Street |
| CUTY: Seattle |
| CORRESPONDENCE |
| CORRESPOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Apple Operating System 7.1 SOFTWARE: Microsoft Word for Apple, Version 5.1a CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMATER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:

CLASSIETCATION NOMBER: US/OB/936,854

CLASSIETCATION 435

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 08/430,633

FILING DATE: 28-APR-1995

APPLICATION NUMBER: US 08/28,397

FILING DATE: 04/28/94

ATTORNEY/AGENT INFORMATION:

NAME: PERKINS, PALTICIA A.

RECISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2612

TELEPHONE: (206)233-0644

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 212 amino acids

TTYPE: maino acids
         51 UNIVERSITY STREET
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein ORIGINAL SOURCE:
                                SEATTLE
WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: 19G1 FC
                                                                                                USA
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COUNTRY: US
ZIP: 98101
                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Patent No. 6100235

GENERAL INFORMATION:
APPLICANT: Yeo, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 586; DB 3; Best Local Similarity 100.0%; Pred. No. 2.5e-62; Matches 110; Conservative 0; Mismatches 0;
                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPHONE: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acids
TOPPLOGY: linear
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USSN 08/410,535
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STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/620,694
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APPLICATION NUMBER: USSN 01
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; IMMEDIATE SOURCE:
; CLONE: 19G1 FC
US-09-022-253-4
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CLASSIFICATION:
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US-09-022-260-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 APELLGGPSVFLFPFRFKDTLMISRTPEVTCVVVDVSHEDPEVFFNWYVDGVEVHNAKTK 73
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Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Aro, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION:
NOWBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 586; DB 3; Length 212; Best Local Similarity 100.0%; Pred. No. 2.5e-62; Matches 110; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
FILING DATE: 7 AUGUST 1995
FILING DATE: 7 AUGUST 1995
                                                                                                                        USSN 08/410,535
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
21P: 98101
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human
IMMEDIATE SOURCE:
                                                       FILING DATE:
CLASSIFICATION:
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CLASSIFICATION:
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INFORTION: No. 6197525el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                         100.0%; Score 586; DB 4; Length 212; 100.0%; Pred. No. 2.5e-62; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOCTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION NUMBER: US/09/022,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PERKING, PATRICIA Anne
REGISTRATION NUMBER: 34,695
REPRENEC/FOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09022257
Patent No. 6197525
                                                                                                                                not relevant
                              TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
              (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 110; Conservative
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LENGTH: 212 amino acids
                                                                                                                                                                   MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                    linear
                                                                                                                                                                                                   ORGANISM: Human
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                IgG1 Fc
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              TELEPHONE:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/0902259
Patent No. 6191104
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Sprigs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 586; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.5e-62;
Matches 110; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DAIL..
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
APPLICATION NUMBER: 23 MARCH 1995
          NAME: PERKIDS, PATRICIA ANDERES SECISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELEPRONE: (206)587-0430
TELEPRONE: (206)587-0430
INFORMATION FOR SEQ ID NO: 4:SEQUENCE CHARACTERISTICS: LENGTH: 212 amino acids TYPE: amino acid STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                ; CLONE: IgG1 FC
US-09-022-260-4
                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seatt
STATE: WA
COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-022-259-4
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76 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPADIEKTISKAK 125
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                                                                                                                      Sequence 6, Application US/09131247
Patent No. 6294170
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Human
US-09-131-247-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                      US-09-131-247-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                       14 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
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                                                                                                                                                                                                                                                                                                                                                                                                 74 PREEQYNSTYRVVSVLIVLHOOMLNGKEYKCKVSNKALPAPIEKTISKAK 123
                                                                                                                                                                                                                                                                                                                                                                            61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 586; DB 2;
100.0%; Pred. No. 2.8e-62;
ive 0; Mismatches 0;
                                                                                                                                                                                                                  100.0%; Score 586; DB 4;
1larity 100.0%; Pred. No. 2.5e-62;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: MEDLEN & CARROLL
220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: CARROLL, PETER G.
RECISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGAR-00371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50, Application US/08595043A Patent No. 5935824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 705-8410
TELERAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
                            not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 110; Conservative
                                        TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: 1961 FC
                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 110; Conserv
TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-595-043A-50
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APPLICANT: BOCALLOW:
APPLICANT: Hershenson, Susan
APPLICANT: Hershenson, Susan
APPLICANT: Hershenson, Michael P.
APPLICANT: Bevilacqua, Michael P.
APPLICANT: Collins, David S.
ITILE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
ITILE OF INVENTION: DISEASES
FILE REPERBACE: A-365F
CURRENT APPLICATION NUMBER: US/09/131,247
CURRENT FILING DATE: 1998-08-07
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-02-10
NUMBER: OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 APELLGGPSVFLFPPFKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Roneo, Charles
APPLICANT: Rolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF SEQUENCES: SECUENCES: SECUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%; Score 586; DB 4; Length 235; Best Local Similarity 100.0%; Pred. No. 2.9e-62; Matches 110; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastERG DOS
SOFTWARE: FastERG TO Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE:
CLASSIFICATION: 514
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us-09-674-857-4.rai

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0
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Best Local Similarity 100.0%; Score 586; DB 2; Length 254;
Bast Local Similarity 100.0%; Pred. No. 3.2e-62;
Matches 110; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00786/247001
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MR-1992
APPLICATION NUMBER: 07/65,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 35,238
TELECHONE: 617-428-0200
TELEFRAX: 617-428-0200
TELEFRAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 and.no acids
TYPE: and.no acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-284-391B-33
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Search completed: June 21, 2002, 08:32:15 Job time: 89 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                           OM protein - protein search, using sw model
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June 21, 2002, 08:37:52; Search time 102.05 Seconds (without alignments) 102.633 Million cell updates/sec Run on:

US-09-674-857-2 580 1 APPVAGPSVFLFPPRPKPTL.......CKVSNKGLPSSIEKTISKTK 109 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|            | Description | g gamma-2 chain | g gamma-4 chain | g gamma- | g gamma-3 chain | g gamma chain C | Ig gamma-1 chain C | g gamma-1 chain | g heavy ch | ъ      | g gamma 2k | g gamma 2a | 6      | Б      | 6      | Ig heavy chain pre | g heavy chain C | Ig gamma-2 chain C | g gamma-1 | 6      | g gamma chain C | g gamma-2 chain | g gamma-3 | g gamma-3 chain | 5    | g gamma-1 | ā      | Ig gamma-2c chain | Ig gamma-1 chain C | Ig gamma-2a chain |
|------------|-------------|-----------------|-----------------|----------|-----------------|-----------------|--------------------|-----------------|------------|--------|------------|------------|--------|--------|--------|--------------------|-----------------|--------------------|-----------|--------|-----------------|-----------------|-----------|-----------------|------|-----------|--------|-------------------|--------------------|-------------------|
|            | Ω           | G2HU            | G4 HU           | A60764   | A23511          | PT0207          | S31866             | GHHU            | 869339     | G3HUWI | 147160     | 147159     | 147162 | 147161 | 147158 | S22080             | C30554          | G2GP               | S31459    | PS0018 | GHRB            | S06611          | G3MSC     | G3MSM           | GIMS | GIMSM     | PC4436 | S00847            | PS0017             | G2MSAB            |
|            | DB :        | -               | ٦               | 7        | 7               | 7               | 4                  | П               | 7          | Н      | 7          | 7          | ~      | 7      | ~      | ~                  | N               | Н                  | ~         | 7      | Н               | 7               | ٦         | 7               | П    | Н         | N      | ~                 | ~                  |                   |
|            | Length      | 326             | 327             | 377      | 377             | 234             | 255                | 330             | 374        | 289    | 328        | 328        | 277    | 328    | 328    | 470                | 308             | 329                | 472       | 333    | 323             | 327             | 329       | 398             | 324  | 393       | 444    | 329               | 326                | 335               |
| %<br>Query | Match       | 98.6            |                 |          |                 |                 | 90.3               |                 |            |        |            |            |        |        | -      |                    | ω,              | ω,                 | ٠         | ö      |                 |                 |           |                 |      |           | 70.7   |                   |                    |                   |
|            | Score       | 572             | 536             | 529      | .529            | 526             | 524                | 524             | 524        | 516    | 457        | 457        | 452    | 441    | 441    | 429                | 425             | 425                | 425       | 423    | 418             | 414             | 0         | 410.5           | 410  | 410       | 410    | 400               | 384                | 383               |
| Result     | No.         | 1               | 7               | ო        | 4               | ហ               | 9                  | 7               | 80         | 6      | 10         | 11         | 12     | 13     | 14     | 15                 | 16              | 17                 | 18        | 19     | 20              | 21              | 22        | 23              | 24   | 25        | 56     | 27                | 28                 | 29                |

| Ig gamma-2b chain | Ig gamma-2b chain | Ig gamma-2a chain | Ig gamma-2a chain | Ig gamma-2a chain | Ig gamma-2b chain | Ig gamma-2a chain | Ig gamma-2a chain | Ig gamma-2a chain | Ig gamma-2b chain | Ig gamma heavy cha | Ig epsilon-chain - | Ig epsilon chain C | Ig gamma-1 chain C | Ig heavy chain pre | Ig mu chain C regi |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| G2MSBM            | G2MS11            | G2MSA             | G2MSAM            | S37483            | S01321            | \$40295           | PS0019            | B30503            | A30503            | 146732             | 136948             | ЕННО               | S14236             | S04845             | S03961             |
| н                 | -                 | -                 | Н                 | 7                 | ~                 | 7                 | 7                 | ~                 | 7                 | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  |
| 405               | 474               | 330               | 399               | 469               | 475               | 446               | 322               | 112               | 88                | 180                | 426                | 428                | 152                | 549                | 457                |
| 0.99              | 0.99              | 65.2              | 65.2              | 65.2              | 63.6              | 63.4              | 59.0              | 53.4              | 47.8              | 43.8               | 29.9               | 29.7               | 29.7               | 26.9               | 26.2               |
| 383               | 383               | 378               | 378               | 378               | 369               | 368               | 342               | 310               | 277               | 254                | 173.5              | 172.5              | 172                | 156                | 152                |
| 30                | 31                | 32                | 33                | 34                | 35                | 36                | 37                | 38                | 39                | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

| RESULT 1 G2HU Ig gamma-2 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000 C;Accession: A93906: A92809: A90752: A93132: A02148                                                                                                                                                                                                                                                                                             |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <br>Riellison, J.; Hood, L. Proced, L. Proced, L. Proc. Nati. Acad. Sci. U.S.A. 79, 1984-1988, 1982 Proc. Nati. Acad. Sci. U.S.A. 79, 1984-1988, 1982 A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A:Reference number: A93906; MUID:82197621 A:Reference number: A93906 |
| <br>A; Residues: 1.326 <ell> A; Residues: 1.326 <ell> A; Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056 A; Note: Lys 326 is probably removed posttranslationally R:Wang, A:C.; Tung, E.; Fudenberg, H.H.</ell></ell>                                                                                                                                                                                                                                                                                 |
| J. Immunol. 125, 1048-1024, 1380<br>A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an<br>A;Teference number: A92809; MUID:81007873<br>A;Contents: myeloma protein Til<br>A;Accession: A92809                                                                                                                                                                                                                                                                                                        |
| <br>A.Molecule type: protein A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <wan> A;Note: Trp-156 is at or near the complement-binding site B;Connell, G.E.; Parr, D.M.; Hofmann, T.</wan>                                                                                                                                                                                                                                                                                                                                    |
| <br>Can. 9. Blocomen. 37, 738.70, 1979 A.Title: The amino acid sequences of the three heavy chain constant region domains of A.Title: The amino acid sequences of the three heavy chain constant region domains of A.Teference number: A90752; MUID:80001357 A.Accession: A90752                                                                                                                                                                                                                                                        |
| A.Molecule type: protein<br>A.Residues: 1-24, E',26-57, EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',1<br>A.Note: this sequence has since been revised<br>R.Hofmann, T.: Parr, D.M.                                                                                                                                                                                                                                                                                                                                          |
| <br>Mol. Immunol. 16, 923-925, 1979 A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli A;Reference number: A93132; MUID:80114419 A.Contants: 2:e                                                                                                                                                                                                                                                                                                                                                     |
| <br>A.Accession: A93132<br>A.Molecule type: protein<br>A.Residues: 238-275 <hof><br/>R.Hofmann, T.; Parr, D.M.</hof>                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <br>submitted to the Atlas, March 1980 A; Reference number: A94591 A; Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268 A; Note: the revised sequence differs from that shown in having 60-Ala and in the amid                                                                                                                                                                                                                                                                                                   |
| <br>ned<br>R:Milstein, C.; Frangione, B.<br>Biochem. J. 121, 217-225, 1971<br>A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.<br>A:Reference number: A90253; MUID:72033500<br>A:Contents: annotation; myeloma protein Sa, disulfide bonds                                                                                                                                                                                                                                                                    |

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C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4 conv A;Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #text_change 23-Jul-1999
C;Date: 28-Dec-1887 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:9577056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Homo sapiens (man)
C.Date: 14-May 1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                           4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                        4 VAGPSVFLFPPKPKPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
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A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                175 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma-3 chain C region (allotype G3m(b)) - human
                                                                         Score 536; DB 1.
Pred. No. 5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.2%; Score 529; DB 2 92.5%; Pred. No. 3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.2%; Score 529; DB 2 92.5%; Pred. No. 3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                        3; Mismatches
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                                                                         92.48;
94.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                            Conservative
                                                                  Query Match
Best Local Similarity
Matches 100; Conserv
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Best Local Similarity
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Matches 98; Conserv
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A; Residues: 1-377 <HUC>
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A.MAP position: 14932.33-14932.33
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap main disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C.Superfamily: immunoglobulin homology < IMA>
F.70-85/Domain: immunoglobulin homology < IMA>
F.739-306/Domain: immunoglobulin homology < IMA>
F.739-306/Domain: immunoglobulin homology < IMA>
F.74/Disulfide bonds: interchain (to light chain) #status experimental
F.70-87/1006,109/Disulfide bonds: #status experimental
F.70-87/1006,109/Disulfide bonds: #status experimental
F.70-87/1006,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F.70-87/1006,109/Disulfide bonds: interchain (to heavy chain) #status experimental
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A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMI>
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A; Accession: A90933
A; Molecule type: DNA
A; Note: the sequence was determined from the germline gene
B; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant
A; Reference number: A90249; MUID:70207560
A; Accession: A90249
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F;134-203/Domain: immunoglobulin homology <IM2>
F;134-203/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;14/Disulfide bonds: interchain (to heavy chain) #status experimental
F;105,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 170
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Pred. No. 1.1e-50;
1; Mismatches 1;
                                                                         6
R; Frangione, B.; Milstein, C.; Pink, J.R.L. Nature 221, 145-148, 1969
A; Title: Structural studies of immunoglobulin R*Reference number: A93157; MUD: 69064124
A; Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                 A)Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
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A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
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98.2%;
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Best Local Similarity 98.2'
Matches 107; Conservative
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A; Accession: A93433
A; Molecule type: DNA
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C;Species: synthetic
A;Note: Homo saphens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: 331866
R;Filpula, D.
Submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: 831866
A;Accession: S31866
A;Accession: S31866
A;Residues: 1-255 <FIL>
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C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: P70207
Mol. Immunol. 28, 319-322, 1991
A.Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A.Reference number: P70207; MUD:91287716
A.Accession: P70207
A.Molecule type: mRNA
A.Refidues: 1-234 *CEHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>
                                                               Gaps
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                                          4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Reywonds: 1mmunglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 AKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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      Indels
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      4;
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Pred. No. 3.5e-46;
5; Mismatches 4
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Pred. No. 6.1e-46;
    4; Mismatches
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86.8%;
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86.0%;
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    Conservative
98;
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Best Local Si
Matches 999
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Griggement creation respins (man)
Cripter 11-20m 1981 sequence. revision 18-40-1982 fetat_change 16-Jul-1999
Cripter 11-20m 1981 sequence. revision 18-40-1982 fetat_change 16-Jul-1999
Cripter 21-20m 1981 sequence. revision 18-40-1982 fetat_change 16-Jul-1999
Cripter 21-20m 1981 sequence. revision 18-40-1982 fetat_change 18-40-123: A02146
Refiliation 18-40-1983 Scafedii Salefy; Boddei; Boddei; Boddei Bodde
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gamma3 hea

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A; Molecule type: protein
A; Residues: 1-289 <FRA>,
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A; Note: this protein lacks most of the V region and all of the CH1 region. Residue 12
A; Note: this protein lacks most of the V region and all of the CH1 region. Residue 12
A; Note: the sequence of residues 42-76 was taken from the reference that follows
B; Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A; Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat
A; Reference number: A92219; MUID: 77118561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein A; Accession: A9219
A; Molecule type: protein A; Residues: 12-97 AIIC>
A; Note: the hinge region in gamma-3 chains is about four times as long as in other gampa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 59-125, EB', 128-226, 228-289 < MOL>
A; Residues: 59-125, EB', 128-226, 228-289 < MOL>
A; Note: this protein lacks most of the V region, all of the CH1 region, and part of the A; Note: this protein lacks most of the V region, all of the CH1 region, and part of the V region, all of the CH1 region, B.C.; Hood, Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletian the A; Reference number: A93915; MUID:82247835
A; Contents: heavy chain disease protein omm
A; Accession: A93915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 12-70;72-114;116-125, E',127-133, L',135-136, E',138, Y',140-154, 'D',156-A; Note: a carboxyl-terminal Lys is removed posttranslationally A;Note: this sequence may represent an allelic form or another gamma chain subclass C;Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                idue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form 1
R;Wolfenstein-Todel, C.; Frandione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of A;Reference number: A90198; MUID:77021516
                                                                                                                                                                                                                                                                                                           C; Species: Homo sapiens (man)
C; Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C; Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C; Accession: A90442; A92219; A90198; A9315; A02149
R; Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A; Title: Primary structure of human gamma3 immunoglobulin deletion mutant: g
A; Reference number: A90442; MUID:81021548
A; Contents: heavy chain disease protein Wis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Gln) #status experimental
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimenta
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
           56 AKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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Pred. No. 4.7e-45;
7; Mismatches 4.
                                                                                                                                                                                                                                                                            Ig gamma-3 heavy chain disease proteins - human
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Best Local Similarity 89.6%;
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C. Superfamally: immunoglobulin C region; immunoglobulin pomology C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F; 20-85/Domain: immunoglobulin homology < IM2> F; 237-206/Domain: immunoglobulin homology < IM2> F; 243-310/Domain: immunoglobulin homology < IM2> F; 243-310/Domain: immunoglobulin homology < IM3>
A;Reference number: A90565; MUID:71064027
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hlschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region precursor - human C; Species: Homo sapiens (man) F sequence_revision 19-Mar-1997 #text_change 01-Dec-2000 C; Accession: S69339; S72664 R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M. Bur. J. Biochem. 229, 54-60, 1995 A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A; Reference number: S69339; MUID:95262687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 PPCPAPELIGGPSVFLFPPKFKDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:27-83,144-204,250-308/Disulfide bonds: #status experimental F:103/Disulfide bonds: interchain (to light chain) #status experimental F:109,112/Disulfide bonds: interchain (to heavy chain) #status experiments F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 AKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Pred. No. 9.8e-46;
6; Mismatches 4;
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St,Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
                                                                                                                                                                                                                                                                A; Contents: annotation; disulfide bonds C; Genetics:
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A; Residues: 1-140, 'C', 142-374 <KH2>
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86.0%;
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98; Conservative
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Best Local Similarity
Matches 98; Conserv
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A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
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A; Status: preliminary
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Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147162
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158; MUID:95015845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA sequences of
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147161
C. gamma 3 chain constant region - pig (fragment)
C. Species: Sus scrofa domestica (domestic pig)
C. Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C. Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb.1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I41158
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mnA
A,Residues: 1-328 <RAC>
A,Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: manAA
A;Residues: 1-277 <KAC>
A;Coss-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQF 124
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J. Immunol. 153, 3555-373, 1994
A.; Title: Five putative subclasses of swine IgG identified from the A;Reference number: 147158; MUID:95015845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.0%; Score 441; DB 2; Length 328; 77.9%; Pred. No. 2.4e-37; ive 12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: IgC4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 452; DB 2;
Pred. No. 1.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 77.9%;
Best Local Similarity 77.9%;
Matches 81; Conservative 1
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Best Local S
Matches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: In 1920 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a SA Reference number: I47158; MUID:95015845
A;Reference number: I47158; MUID:95015845
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 cKAC>
A;Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                             14/30 c) Species: Sus scrofa domestic pig)
C; Accession: 147160
R; Kacskovics, I: Sun, J: Butler, J.E.
J: Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a shacession: 147160
A; Reference number: 147160
A; Reference number: 147160
A; Returs: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-328 < KAC>
A; Cross-references: EMBL: U03780; NID: 9433125; PIDN: AAA52218.1; PID: 9433126
C; Genetics:
A;                                                                                                                                                                                                                                                                                                                                                                                                                                   Ø
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66 NSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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Best Local Similarity 78.8%; Pred. No. 5.7e-39;
Matches 82; Conservative 13; Mismatches 9;
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Best Local Similarity
Matches 82; Conserv
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N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: $22080; $06610; A31303
R;Sanders, PG.
Submitted to the EMBL Data Library, November 1991
A;Reference number: $22080
A;Retaus: preliminary
A;Molecule type: mRNA
A;Retaus: preliminary
A;Molecule type: mRNA
A;Retaus: Dreliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Residues: 1-470 <SAN>
A;Residues: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma, A;Reference number: $06610; MUID:90097956
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Itile: Five putative subclasses of swine IgG identified from the CDNA sequences of a :A; Title: Five putative subclasses of swine IgG identified from the CDNA sequences of A; Reference number: I47158; MUID:95015845
A; Recession: I47158
A; Recession: I47158
A; Residue: pre-iminary; translated from GB/EMBL/DDBJ
A; Residues: 1.328 < KAC>
A; Residues: 1.328 < KAC>
A; Cross-references: EMBL:U03778; NID:9433121; PIDN:AAA52216.1; PID:9433122
A; Genetics:
A; Genetic
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A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: 91ycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 76.0%; Score 441; DB 2; Similarity 77.9%; Pred. No. 2.4e-37; 81; Conservative 12; Mismatches 11.
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Matches 79; Conservative
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Best Local S
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NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCETONING NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
ZIP: 02173
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
GY: linear
                                                                                                                                                                                                                                                                         CITY: Lexington STATE: MA
USA
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: ami
TOPOLOGY:
                                                                                                                                                                                US-08-444-644-30
                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, p
Sequence 4, p
Sequence 4, p
Sequence 4, p
Sequence 4, p
Sequence 4, p
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Sequence 23,
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Sequence 2,
Sequence 2,
                                                                             US-09-674-857-1
581
1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKAK
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                                                  June 21, 2002, 08:30:46; Search time 77.71 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-477-460B-2
US-08-379-516-2
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US-09-485-737B-90
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US-08-232-539D-55
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US-07-934-373C-23
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PCT-US93-07832-23
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US-08-485-372A-2
US-09-409-006A-2
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-08-936-854-4
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US-08-477-460B-4
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US-09-409-006A-4
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US-09-329-916-4
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                                                                                                                                   231628 seqs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Maximum DB seq
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Perfect score:
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Patent No. 6015555
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                      Sequence 43, A Sequence 8, A Sequence 43, A Sequence 11, Sequence 7, A Sequence 7, A
                                                                                                                                                                               Sequence 43,
Sequence 43,
Sequence 43,
    Sequence 4
Sequence 4
Sequence 4
Sequence 5
Sequence 5
Sequence 3
Sequence 3
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COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
US-09-022-253-4
US-09-022-260-4
US-09-022-257-4
US-09-022-257-4
US-08-595-043A-50
US-09-118-950-33
US-09-118-950-33
US-08-218-950-33
US-08-459-512-43
US-08-459-512-43
US-08-460-132-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: 05 07/800,458
FILING DATE: 26 NOV-1991
PRIOR APPLICATION DATA: 75 NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA: 75 NOV-1991
FILING DATE: 07-SEP-1990
ATTORNEY/AGENT: 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Hamilton, Brook,
Two Militia Drive
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Sequence 2, Application US/08477460B

Sequence 2, Application US/08477460B

Patent No. 6034223

GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
ATILE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-1gG2 IMMUNOCONJUGATES, AND USES THEREOF
CURRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: 30 Rockefeller Plaza
CITY: New York
STATE: New York
STATE: New York
                                                             1 APPVAGPSVFLFPPKRKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                 1 APPVAGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                                                                                                                                         Indels
                                                                                                                               61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN RELEASE #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,460B
FILING DATE: 0'-JUN-1995
CLASSIFICATION NUMBER: US 07/927,931
FILING DATE: 0'-AUG-1992
APPLICATION NUMBER: US 07/927,931
FILING DATE: 0'-AUG-1992
APPLICATION NUMBER: US 07/927,931
FILING DATE: US 07/927,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 554; DB 3; L
Pred. No. 5.9e-56;
5; Mismatches 2;
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Best Local Similarity 93.6%;
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                     RESULT 3
US-08-477-460B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-477-460B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30, Application US/08232246A
Patent No. 6329508
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTHBODY NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    Gaps
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                                                                                                                        Score 554; DB 3; Length 109;
Pred. No. 9.7e-57;
5; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                  61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                              Query Match 95.4%; Score 554; DB 4; Length 10 Best Local Similarity 93.6%; Pred. No. 9.7e-57; Matches 102; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
ATPORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Wagner, Richard W.
REGISCHRATION NUMBER: 34,480
REFENCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                     Query Match 95.4%;
Best Local Similarity 93.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 109 amino acids
amino acid
                              internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02173

    MOLECULE TYPE:
    FRAGMENT TYPE:
US-08-444-644-30
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-08-232-246A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
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Pred. No. 5.9e-56;
5; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TILE OF INVENTION: C14-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37690-II-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,476,227
FLING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08485372A Patent No. 6187748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                  95.4%;
  TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
                                                                                       LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 93.6
Matches 102; Conservative
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                              ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-09-329-916-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo sapien
                                                                                                                                                                         protein
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                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: prote ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                       Query Match
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                 Sequence 1, Application US/08379516
Patent No. 6083478
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Allaway, Graham P.
APPLICANT: Allaway, Graham P.
APPLICANT: Allaway, Graham P.
APPLICANT: MIGHON, Paul J.
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT PILING DATE: 1996-06-10
EARLIER APPLICATION NUMBER: PCT/US93/07422
EARLIER FILING DATE: 1993-08-06
EARLIER FILING DATE: 1993-08-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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Pred. No. 5.9e-56;
5; Mismatches 2; Indels
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REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,460
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6177549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TORNEY/AGEN1 1..... NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.4%;
Best Local Similarity 93.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens US-08-379-516-2
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CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
US-08-379-516-2
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APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 30 Rookefeller Plaza
CITY: New York
CJUNTRY: New York
CJUNTRY: USA
ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                     61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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Pred. No. 5.9e-56;
5; Mismatches 2; Indels
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9560
TELERA: (212) 977-9560
TELERA: (212) 977-9509
TELERA: (212) 977-9509
TELERA: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
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Patent No. 6034223
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
                                                                                                                                                                       Sequence 2, Application PC/TUS9307422 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 93.69
Matches 102; Conservative
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PCT-US93-07422-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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                                                                                                                               RESULT 8
PCT-US93-07422-2
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US-08-477-460B-4
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APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: OAG-SEPTIDYL MOISTY-CONJUGATED
TITLE OF INVENTION: CO4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                     Length 432;
                                                                                                                                                                                                                                       61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                 95.4%; Score 554; DB 4; Length 432; 93.6%; Pred. No. 5.9e-56; tive 5; Mismatches 2; Indels
                                                                                Score 554; DB 4; Length 43
Pred. No. 5.9e-56;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41215-A-PCT/JPW/AJM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/409,006A FILING DATE: 29-SEP-1999 CLASSIPICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/927,931 FILING DATE: 07-AUG-1992 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
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Patent No. 6342586
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4121:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 977-9550
TELEFX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                95.4%;
                                                                                                                  Matches 102; Conservative
CELL TYPE: lymphocyte US-08-485-372A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                            Query Match
Best Local Similarity
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Best Local Similarity
Matches, 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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Sequence 4, Application US/09329916
Patent No. 6177549
GENERA INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                                                                                                                                  Length 530;
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Pred. No. 7.6e-56;
5; Mismatches 2; Indels
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEFAX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/477,460
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGGNT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTER.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
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STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                               95.4%;
93.6%;
             SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 530
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 93.6
Matches 102; Conservative
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                                                                                                                                            ; ORGANISM: Homo sapiens
US-08-379-516-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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US-09-329-916-4
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                                                                                                                    TYPE: PRT
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Patent No. 6083478
GENERAL INFORMATION:
APPLICANT: Allaway, Graham P.
APPLICANT: Allaway, Graham P.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/08/379,516
CURRENT FILING DATE: 1996-06-10
EARLIER FILING DATE: 1996-06-10
EARLIER FILING DATE: 1992-08-06
EARLIER FILING DATE: 1992-08-07
EARLIER FILING DATE: 1992-08-07
          NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUTCATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/477,460B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LELETAX: (212) 977-9550
TELETAX: (212) 977-9550
TELEX: 42553 COOP UI
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: urver
TITLE OF INVENTION: NON-PEPTIDYL TITLE OF INVENTION: CD4-GAMMA2 AN NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                           10112
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Sequence 4, Application US/09409006A
Patent No. 6342586
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 ROCKefeller Plaza
CITY: New York
STATE: New York
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GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 977-9550
TELERAX: (212) 977-9809
TELEEX: 422523 COOP UI
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL TYPE: lymphocyte US-09-409-006A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                           USA
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                                           US-09-409-006A-4
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PCT-US93-07422-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                           61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                     Indels
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
  Pred. No. 7.6e-56;
5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,372A
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                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08485372A Patent No. 6187748 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
Best Local Similarity 93.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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New York
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                                                                                                                                                                                                                                                                                US-08-485-372A-4
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1 APPVAGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIPECATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTATION NUMBER: 40,378
REGISTATION NUMBER: 909871
TELECOMMUNICATION INFORMATION:
TELEFAN: 415/95-981
TELEFAN: 415/95-981
TELEFAN: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 21, 2002, 08:32:13 Job time: 87 sec
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Best Local Similarity 92.73
Matches 101; Conservative
       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: Linear
US-08-788-800-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.4%; Score 554; DB 5; Length 530; 93.6%; Pred. No. 7.6e-56; tive 5; Mismatches 2; Indels
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Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bedinar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLINE CALLS: 1933000
CLASSIFICATION:
PRIOR APPLICATION DATA:
PPIOR APPLICATION DATA:
FILING DATE: 07-040-1992
ATORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 28 678
REFERENCY/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: 42253 COPP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TYPE: amino acid
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC COMPATISE
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...uresse: ...uress: ...uress: ...uresse: ...aresse: ..
                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MODECULE TYPE: CDNA ORIGINAL SOURCE: ORGANICA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 95.4
Best Local Similarity 93.6
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE: lymphocyte PCT-US93-07422-4
                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                              New York
                                   New York
                                                                                                             USA
                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-788-800-12
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0; Gaps

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June 21, 2002, 08:30:46; Search time 102.05 Seconds (without alignments) 102.633 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                 Run on:
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US-09-674-857-1 581 1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKAK 109 283138 Total number of hits satisfying chosen parameters: 283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Sequence: Scoring table: Searched: Title:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description         | 9 gamma - 1 c<br>9 gamma - 3 c<br>9 gamma - 3 c<br>9 gamma - 2 a<br>9 gamma - 2 c<br>9 gamma - 3 c<br>9 gamma - 3 c<br>9 gamma - 1 c<br>9 gamma - 1 c<br>9 gamma - 1 c                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Ig gamma-2a chain<br>Ig gamma-2b chain |
|---------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------|
| SUMMARIES           | G2HU<br>PT0207<br>S81866<br>S31866<br>G31866<br>G4HU<br>G4HU<br>G4HU<br>G40764<br>A23511<br>G3147160<br>147160<br>147161<br>147161<br>147161<br>147162<br>G3147<br>G3161<br>G3161<br>G316<br>G316<br>G316<br>G316<br>G316<br>G3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | G2MSBM<br>G2MSBM                       |
| DB                  | 10410100100000000110110011001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | -<br>-                                 |
| Length 1            | 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 405                                    |
| %<br>Query<br>Match |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 65.7                                   |
| Score               | 558<br>543<br>5443<br>55443<br>55443<br>6584<br>6445<br>6445<br>6445<br>6445<br>6445<br>6445<br>6445                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 382                                    |
| Result<br>No.       | 100 4 5 9 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 8 7 9 9 8 7 9 9 9 8 7 9 9 9 9 | 29                                     |

| Ig gamma-2b chain<br>Ig gamma-1 chain C | Ig gamma-2a chain<br>Ig gamma-2a chain | 19 gamma - 2a chain<br>19 gamma - 2b chain | 19 gamma-za chain<br>Ig gamma-za chain | Ig gamma-2a chain<br>Ig gamma-2b chain | Ig gamma heavy cha<br>Ig epsilon-chain - | Ig epsilon chain C<br>Ig gamma-1 chain C | Ig heavy chain pre<br>Ig epsilon chain C |
|-----------------------------------------|----------------------------------------|--------------------------------------------|----------------------------------------|----------------------------------------|------------------------------------------|------------------------------------------|------------------------------------------|
| G2MS11<br>PS0017                        | G2MSA<br>G2MSAM                        | S3/483<br>S01321                           | S40295<br>PS0019                       | B30503<br>A30503                       | 146732<br>136948                         | ЕННU<br>S14236                           | S04845<br>EHRT                           |
| 42                                      |                                        | 7 77 7                                     | 7 7                                    | 0 0                                    | 77                                       | 7                                        | 7.5                                      |
| 326                                     | 0 6 6 6                                | 475                                        | 322                                    | 112<br>88                              | 180<br>426                               | 428                                      | 549<br>429                               |
| r. 4.                                   | ممن                                    | بنور                                       | 3 %                                    |                                        | ۵. ه.                                    | ۲. 6.                                    | ٠<br>۳.                                  |
| 65                                      | 6.40                                   | 63.4                                       | 28                                     | 53                                     | 28                                       | 28                                       | 27                                       |
| 382                                     | 377                                    | 368                                        | 387<br>339                             | 309<br>276                             | 249<br>167.5                             | 166.5<br>162                             | 157<br>153                               |
| 30                                      | 33.7                                   | 3.5                                        | 37                                     | 8 6<br>6 6                             | 40<br>41                                 | 4 4<br>2 8                               | 44<br>45                                 |

## ALIGNMENTS

| Cipaces 10-App-1191 Resequence_EveVision 13-Jun 13-Jun 1918   FREILISON, J.; Hood, L. Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982 A. Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A. Reference number: A93906, MUD: 8219761 A. Reference number: A93906, MUD: 8219761 A. Reference number: A93906 A. Molecule type: DNA A. Residues: 1.350 CELL. A. Title: The principally removed posttranslationally B. Molecule type: DNA A. Title: The principally removed posttranslationally A. Title: The principally removed posttranslationally B. Mannol. 125-1048-1080; MUID: 8210783 A. Title: The principal removed posttranslationally A. Molecule type: protein Til. A. Title: The amino acid sequences of the three heavy chain constant region domains of A. Title: The amino acid sequence of the sequence of the protein Til. A. Title: The amino acid sequence of residues 381-391 of human immunoglobuli A. Residues: 124, E., 25-57, EV, 60-85;132-171, 'ZZZ', '175, 'B', '177-193, 'D', '195-196, 'Q', '1 A. Residues: 124, E', 25-55, 1979 A. Title: The amino acid sequence of residues 381-391 of human immunoglobuli A. Residues: 324-325 4095 A. A. Reference number: A93132; MUD: 80114419 A. Reference on the amino acid sequence of residues 25, 59, 60, and 264-268 A. Reference on the amino acid sequence of residues 25, 59, 60, and 264-268 A. Reference on the amino acid sequence differs from that shown in having 60-Aia and in the amid new submitted to the Anlas, March 1980 A. Reference on where: A Brandone B. B. Reference on the revised sequence B. B. Contents: amontation: 21e, revisions to residues 25, 59, 60, and 264-268 A. Reference on the revised sequence B. B. Raist |
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Gaps

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A. Residues: 1-330 < ELL>
A. Rotoss-references: EMBL: 21/370
A. Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker A. Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker A. Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker a. Note: Lys. 330 is removed after translation
R. Harris, L.J.
Submitted to the EMBL Data Library, October 1992
A. Reference number: S33804
A. Residues: 2-330 < HAR.
A. Residues: 2-330 < HAR.
A. Residues: 2-330 < Human immunoglobulin gamma genes: implications for evolution of A. Reference number: S33887; MUID: 83001943
A. Reference number: S33887; MUID: 83001943
A. Residues: 88-113;235-330 < TAR.
A. Residues: B8-113;235-330 < TAR.
A. Residues: B8-113;235-330 < TAR.
A. Residues: B8-113;235-330 < TAR.
A. Residues: BA. Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma Biochemistry 9, 316-3170, 1970
A. Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq A. Contents: myeloma protein Eu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 1-96, R', 98-135 <CUN>
A; Residues: 1-96, R', 98-135 <CUN>
A; Note: this sequence has the Glm(3) marker, 97-Arg
B; Note: this sequence has the Glm(3) marker, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A; Contents: Eu
                                    R;Filpula, D. submitted to the EMBL Data Library, February 1993 submitted to the EMBL Data Library, February 1993 A;Description: Screeing method for protein-protein interactions of cloned gene A;Reference number: S31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Spate: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C; Accession: A93433; S1861; S38687; B90563; A90564; B91668; A91723; A02146
R; Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A; Reference number: A93433; MUID:82274238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Reywords: immungalbulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.5%; Score 543; DB 4; L
Best Local Similarity 90.4%; Pred. No. 6.8e-47;
Matches 103; Conservative 2; Mismatches 3;
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A;Molecule type: protein
                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-255 <FIL>
                                                                                                                                                                                            A; Accession: S31866
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R; Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A; Title: Structural studies of immunoglobulin G.
A; Reference number: A93157; MUD:69064124
A; Contents: annotation; Sa, disulfide bonds
C; Genetics:
A; Ge
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C;Species. synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan.1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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ف
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin
F; 48-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 554; DB 1; Length, 32
Pred. No. 7.2e-48;
5; Mismatches 2; Indels
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Best Local Similarity 93.6%;
Matches 102; Conservative
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Matches 104; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: PT0207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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A,Molecule type: DNA
A,Residues: 1-372 <ELLD.
A)Residues: 1-372 <ELLD.
A)Rote: the sequence was determined from the germline gene
B,Note: the sequence was determined from the germline gene
B,Note: the sequence was G.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
B,Till: Human immunoglobulin sublclasses. Partial amino acid sequence of the constan A,Reference number: A90249; MUID:70207560
A,Reference number: A90249; MUID:70207560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C. Superfamily: immunoglobulin C region; immunoglobulin homology C: Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F: 20-85/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-4 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Decies: 0.2-Apr-1982 #sequence_revision 02-Apr-1982 #sequence_revision 02-Apr-1983; A90249; A02150 C;Accession: A90933; A90249; A02150 DNA 1; 11-18, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:240-307/Domain: immunoglobulin homology <IM3>
F:140-1307/J-130-1247-305/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 PPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 543; DB 2; Length 37
Pred. No. 1.1e-46;
2; Mismatches 3; Indels
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Pred. No. 1.8e-46;
3; Mismatches 2;
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A;Map position: 14432.33-14432.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit
                                                                                                                                                                      A,Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
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95.3%;
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Best Local Similarity 90.4%;
Matches 103; Conservative
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Best Local Similarity 95.3
Matches 101; Conservative
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A; Residues: 1-30;81-326 <PIN>
                                                                                            A; Molecule type: mRNA
A; Residues: 1-374 <KHA>
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
         A; Accession: S69339
A; Status: preliminary
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Ascession: B91686
Ascessio
A; Residues:. 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
                                         A; Note: this sequence has the Gim(non-1) markers, 239-Giu and 241-Met K; Ponsting1, H; Hischmann, W. Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A; Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)
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A.Introns: 99/1; 114/1; 224/1
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kind position: 14932.33-14932.33
A.Introns: 99/1; 114/1; 224/1
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kind disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into its Superfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM2>
F;21-85/Domain: immunoglobulin homology <IM2>
F;21-85/144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;109,112/Disulfide bonds: interchain (covalent) #status experimental
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C; Species: Homo sapiens (man)
C; Sate: 19-War-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S69339; S72664
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
Eur. J. Biochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A; Reference number: S69339; MUID:95262687
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Pred. No. 9.2e-47;
2; Mismatches 3;
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Best Local Similarity 90.4%;
Matches 103; Conservative ;
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S69339
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consists of two identical light (

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C; Species: Homo sapiens (man)
C; Date: 31-Dec-1979 #sequence_revision_23-Oct-1981 #text_change 16-Jul-1999
C; Accession: A90442; A9219; A90198; A93915; A02149
B; Frangione, B.; Rosenwasser, E.; Peralli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A; Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea A; Reference number: A90442; MUID: 81021548
A; Contents: heavy chain disease protein Wis
A; Accession: A90442
A; Molecule type: protein
A; Residues: 1-289 <FRA>
A; Residues: 1-289 <FRA>
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch A; Note: the sequence of residues 42-76 was taken from the reference that follows
B; Note: the sequence of residues 42-76 was taken from the reference that follows
B; Note: the sequence of residues 42-76 was taken from the reference that follows
B; Note: the sequence of residues 2-76 was taken from the reference that follows
B; Note: the sequence of residues 3. 1977
B; Diol. Chem. 252, 883-889, 1977
A; Title: Primary structure of the 'hinge' region of human 1gG3. Probable quadruplicat
A; Rocession: A92219
A; Mulecule type: protein
A; Residues: 12-97 <AMIC>
A; Note: the hinge region in gamma-3 chains; sabout four times as long as in other games and a protein and a part for a far a position of a part for miton and a position and a part for a far a far a position and a part for a far a 
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A; Residues: 59-125, 'EB', 128-226, 228-289 < WOL>
A; Residues: 59-125, 'EB', 128-226, 228-289 < WOL>
A; Residues: 59-125, 'EB', 128-226, 228-289 < WOL>
A; Note: this protein lacks most of the V region, all of the CH1 region, and part of the R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, A; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, A; Accession and heavy chain disease in man: CDNA sequence supports partial gene deletine A; Reference number: A93915, WID: 81247835
A; Contents: heavy chain disease protein Own
A; Accession: A93915
A; Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-180 Contents: The heavy chain disease protein wis is shown.
C; Genetics: The heavy chain disease protein Wis is shown.
C; Genetics: GDB: 119339; OMIM: 147120
A; Map position: 14q32.33-14q32.33
A; Cross-references: GDB: 119339; OMIM: 147120
A; Map position: 14q32.33-14q32.33
C; Superfamily: immunoglobulin homology
C; Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F; 203-270/Domain: immunoglobulin homology cime experimental
F; 6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in R; Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A; Fitle: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A; Reference number: A90198; MUID:77021516
A; Contents: heavy chain disease protein Zuc, partial sequence corresponding to residute A; Accession: A90198
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QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                      86.7%; Score 504; DB 1; Lalarity 86.8%; Pred. No. 6.3e-43; Conservative 9; Mismatches 5;
                                                                                                                                                                                                                                                    Ig gamma-3 heavy chain disease proteins - human
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Best Local Similarity
Matches 92; Conserv
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C;Genetics:
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C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
                                      Gaps
63
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4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
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A;Cross-references: GDB:119339; OMIN:147120
A;Map position: 14q32.33
A;Introns: 96/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin homology C;Keywords: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-377 <HUC>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMM>
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Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin 1989
A;Feference number: A60764; MUID:90007613
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Pred. No. 8.6e-45;
4; Mismatches 5;
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1 Similarity 91.5%;
97; Conservative
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Best Local Similarity
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Les 97; Conserv
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A; Residues: 1-377 <HUC>
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of swine IgG identified from the cDNA sequences of
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C; Accession: I47161
R; Kacskovics, I.; Sun, J.; Butler, J.E.
J; Immunol: I53, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA seque A; Reference number: I47161
A; Reference number: I47161
                                  Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Bate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Bate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Fitle: Five putative subclasses of swine IgG identified from the cDNA sequence number: 147162
A;Accession: 147162
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Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 *sequence_revision 21-Feb-1997 *text_change 21-Jan-2000
C;Accession: I47158
                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
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A;Molecule type: mnnA
A;Residues: 1-328 <KAC>
A;Residues: EBBL:U03781; NID:q433127; PIDN:AAA52219.1; PID:g433128
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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Pred. No. 7.7e-38;
1; Mismatches 9;
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Best Local Similarity 77.9%;
Matches 81; Conservative 1
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CyAccession: 147160
Fixessvics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the CDNA sequences of A;Reference number: 147158; MUID:95015845
A;Accession: 14716
A;Acc
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                                                                                                                                                                             g gamma 2b chain constant region - pig (fragment); Species: Sus scrofa domestica (domestic pig); bate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000; Accession: 147160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Species: Sus scrots domestics (domestic pig)
C; Species: Sus scrots domestics (domestic pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-200(
C; Accession: 147159
R; Raskovics, I.; But, J.; Butler, J.E.
A; Title: Five putative subclasses of swine IgG identified from the CDNA sec A; Reference number: 147159
A; Accession: 147159
A; Accession: 147159
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-328 < KAC>
A; Residues: 1-328 < KAC>
C; Genetics: EMBL: U03779; NID: 9433123; PIDN: AAA52217.1; PID: 9433124
C; Genetics: 1-328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 GPSVFIFPPRPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: immunoglobulin C region; immunoglobulin homology 133-202/Domain: immunoglobulin homology <IMM>
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138 QFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183
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78.8%; Pred. No. 3e-3
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Best Local Similarity 78.8%
Matches 82; Conservative
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Mylternate names: Ig gamma-1 chain C region (clone 8.10)

Species: Ig gamma-1 chain C region (clone 8.10)

Species: Ig gamma-1 chain C region (clone 8.10)

C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C; Accession: S22080; S06610; A31303

R; Sanders, P.G.

submitted to the EMBL Data Library, November 1991

R; Reference number: S22080

A; Reference number: S2080

A; Reference serior: S2080

A; Residues: 1-470 < SAN>

A; Coss references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440

R; Symons, D.B.A.; Clarkson, C.A.; Beale, D.

Mol. Immunol. 26, 841-850, 1989

A; Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamm
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A.Title: Five putative subclasses of swine IgG identified from the CDNA sequences of a A.Fatler: Five putative subclasses of swine IgG identified from the CDNA sequences of A.Faccession: I47158
A.Accession: IA7158
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C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F; 161-225/Domain: immunoglobulin homology <IMM>
F; 318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 142-470
A; Cross-references: EMBL:X16701
A; Note: the sequence was determined from the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 76.1%; Score 442; DB 2; 1 Similarity 77.1%; Pred. No. 1.2e-36; 81; Conservative 13; Mismatches 11;
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Best Local Similarity
Matches 81; Conserva
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GenCore version 4.5
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OM protein - protein search, using sw model

June 21, 2002, 08:36:16; Search time 48.19 Seconds (without alignments) 87.579 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-674-857-1 581 1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKAK 109

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | Description           | P01859 homo sapien | homo      | homo      | homo      | P20761 rattus norv | P01862 cavia porce | orycto   | mus       | P03987 mus musculu | P01868 mus musculu | P01869 mus musculu | P20762 rattus norv | P01864 mus musculu | P01866 mus musculu | P01867 mus musculu | P20759 rattus norv | P01863 mus musculu | P01865 mus musculu | P20760 rattus norv | P01854 homo sapien |         | P20768 suncus muri | P01879 oryctolagus | homo      | 0          | mus n     | homo sa   |           | 7 mesocr  | P01872 mus musculu | 3 mus      | 13 mus     | P20765 mus spretus |
|-----------|-----------------------|--------------------|-----------|-----------|-----------|--------------------|--------------------|----------|-----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------|--------------------|--------------------|-----------|------------|-----------|-----------|-----------|-----------|--------------------|------------|------------|--------------------|
| SUMMARIES | ID                    | GC2_HUMAN          | GC1_HUMAN | GC4_HUMAN | GC3_HUMAN | GCB_RAT            | GC2_CAVPO          | GC_RABIT | GC3_MOUSE | GC3M_MOUSE         | GC1_MOUSE          | GC1M_MOUSE         | GCC_RAT            | GCAB_MOUSE         | GCB_MOUSE          | GCBM_MOUSE         | GC1_RAT            | GCAA_MOUSE         | GCAM_MOUSE         | GCA_RAT            | EPC_HUMAN          | EPC_RAT | MUC_SUNMU          | ALC_RABIT          | KAC_HUMAN | MUCB_HUMAN | EPC_MOUSE | MUC_HUMAN | LAC_CHICK | MUC_MESAU | MUC_MOUSE          | MUCM_MOUSE | LAC1_MOUSE | LAC5_MUSSP         |
|           | DB                    | -                  |           |           |           |                    |                    |          |           |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |         |                    |                    |           |            |           |           |           |           |                    |            | Н,         |                    |
|           | Query<br>Match Length | 326                | 330       | 327       | 290       | 333                | 329                | 323      | 329       | 398                | 324                | 393                | 329                | 335                | 336                | 405                | 326                | 330                | 399                | 322                | 428                | 429     | 457                | 299                | 106       | 391        | 421       | 454       | 103       | 454       | 455                | 476        | 105        | 105                |
|           | Ouery<br>Match        | 95.4               | ω.        | a         |           | 72.3               | 71.8               | 71.1     | 70.7      | 70.7               | 68.2               | 68.2               | 57.5               | 65.7               | 65.7               | 65.7               | 65.4               | 64.9               | 64.9               | 58.3               | 28.7               | 26.3    | 26.3               | 24.0               | 23.9      | 23.9       | 23.8      | 23.8      | 22.7      | 22.7      | 22.7               | 22.7       | 21.9       | 21.8               |
| •         |                       | . 4                |           |           |           |                    |                    |          |           |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |         |                    |                    |           |            |           |           |           |           |                    |            |            |                    |
|           | Score                 | 554                | 543       | 540       | 20        | 42                 | 41                 | 41       | П         | 410.               | 36                 | 39                 | 39.                | 38                 | 38                 | 382                | 38                 | 37,                | 37.                | 33                 | 166.               | 15      | 15                 | 139.               | 13        | 13         | 13        | 13        | 13        | 13        | 13                 | 13         | 127.5      | 126.               |
|           | Result<br>No.         | 1                  | 7         | е         | 4         | S                  | 9                  | 7        | 80        | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21      | 22                 | 23                 | 24        | 25         | 56        | 27        | 28        | 29        | 30                 | 31         | 32         | 33                 |

| PO1874 canis famil P20764 mus musculu P20764 mus musculu P04988 oryctolagus P04221 oryctolagus P01877 homo sapien P20758 gorilla gor P01876 homo sapien P1814 homo sapien P1814 homo sapien P01847 oryctolagus P01847 oryctolagus P01878 mus musculu |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| MUC_CANFA<br>LAC5_MOUSE<br>MUC_RABIT<br>MUC_RABIT<br>ALC2_HUMAN<br>ALC1_GORGO<br>ALC1_GORGO<br>ALC1_HUMAN<br>LAC_HUMAN<br>LAC_HUMAN<br>LAC_RABIT<br>KAC4_RABIT<br>ALC_MOUSE                                                                          |
| напанананан                                                                                                                                                                                                                                          |
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# ALIGNMENTS

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REMOVED POST-TRANSLATIONALLY (PROBABLE).

S -> A (IN MYELOMA PROTEINS TIL & ZIE).

TYTIG-VARA.003889.

C -> S (IN REF. 3).

8310878C6878CF9C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; Biochem, J. 121:217-225(1971).
                                                                                                                                                                                                  MEDLINE-9525298; PubMed-7737190; Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri "Characterization of the two unique human anti-flavin monoclonal
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Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
                                                                        revisions TO 25; 59; 60 AND 264-268 (ZIE). Hofmann T., Parr D.M.;
                                                                                                                              Submitted (MAR-1980) to the PIR data bank.
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Eur. J. Biochem. 228:886-893(1995).
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MEDLINE=72033500; PubMed=4940472;
immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003609; Ig_like.
Fram; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SWART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
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1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
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Query Match
Best Local Similarity 93.65
Matches 102; Conservative

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111 APPVAGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 170
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Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Ikule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE-83289131; PubMed-6884994; Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin igGl KOL, I."; Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure Of a human gamma G-immunoglobulin. VII. Pacid sequence of heavy-chain cyanogen bromide fragments HI-H4.";
Biochemistry 9:3161-3170(1970).
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Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-77070269; PubMed-826475;
Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a
                                       REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                         SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE=71064025; PubMed=5530842;
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                                                                 "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";
Blochemistry 20:2361-2370(1981).
HISCELLANBOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 219-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.

--- MISCELLANBOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35.116,198,269 & 272.

--- MISCELLANBOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 15.116,198,269 & 272.

--- MISCELLANBOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155,166,177,195,198,269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
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R PDB; IFC1; 15-JUL-92.

PDB; 1FC2; 15-JUL-92.

MIM; 147100; ...

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003597; Ig_c1.

R InterPro; IPR003597; Ig_like.

R Pfan; PP00047; Ig; 3.

R SMART; SM00410; IG_like; 1.

R SMART; SM00407; IGc1; 2.

R PROSITE; PS00290; IG_MHC; 2.

M Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; 30. structure.
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R -> R (IN GlM(3) MARKER).

/FTId-VAR_003886.

D -> E (IN GlM(NON-1) MARKER).

/FTId=VAR_003887.

L -> M (IN GlM(NON-1) MARKER).

/FTId=VAR_003888.
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INTERCHAIN (WITH HEAVY CHAIN)
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                             X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; Pubmed-7236608;
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CH3.
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MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Blisson J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
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Pred. No. 2.3e-47;
2; Mismatches 3; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig gamma-4 chain C region.
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PIR; A02150; G4HU.
HSSP; P01842; 7FAB.
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MEDLINE-81021548; PubMed=6774747;
Frangione B. Rosenwasser E., Prealli F., Franklin B.C.;
Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Franglone B., Franklin E.C.;
Mrinary structure of the 'hinge' region of human 1gG3. Probable quadruplication of a 15-amino acid residue basic unit.";
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-3 chain C region (Heavy chain disease protein) (HDC).
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Wolfenstein-Todel C., Franglone B., Prelli F., Franklin E.C.;
"The amino acid sequence of 'heavy chain disease' protein 2UC.
Structure of the Fc fragment of immunoqlobulin G3.";
Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH A LIGHT CHAIN)
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Pred. No. 4.5e-47;
3; Mismatches 2; Indels
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MEDLINE-§2247835; Pubmed-6808505;
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  MIM: 147130; -
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
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Matches 101; Conservative
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                                                                                                                                                           -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
AND ALLO F THE CHI REGION.
-!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
GAMMA-3 HARVY CHAINS.
-!- GAMMA-3 HARVY CHAINS.
-!- MISCELLANEOUS: DISEASE PROTEIN OWM MAY REPRESENT AN ALLELIC FORM
OR ANOTHER GAMMA CHAIN SUBCLASS.
-!- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
SEGMENT (12-28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A02149; G3HUWI.
HSSP: P01857; IFC1.
MIM; 147120.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_C1.
InterPro; IPR003607; Ig_L1.
Ffan; FM0047; Ig_ 2.
SMART; SM00410; IG_L1.
FROSITE; P800209; IG_L1.
PROSITE; P800209; IG_L1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
DOMAIN 12 73 HINGE.
                                                     PUTOC. NATI. ACAG. SCI. U.S.A. 79:3260-3264(1982).

-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.

N-LINKED (GLCNAC. )

INTERCHAIN (WITH HEAVY CHAIN DIMER).

lexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin B.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
gene deletion model."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REMOVED POST-TRANSLATIONALLY
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/FTIG=VAR_003890.
P -> L (IN OMM).
/FTIG=VAR_003891.
F -> Y (IN OMM).
/FTIG=VAR_003892.
/FTIG=VAR_003893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HINGE.
CH2.
CH3.
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289
43
58
73
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                          GC2_CAVPO
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"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
"Gene 74.473-482(1988).
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74.473-482(1988).
PIR: PS0018; PS0018
HSSP; P01842; 7FAB.
HSSP; P01842; 7FAB.
InterPro: IPR003606; Ig_MHC.
InterPro: IPR003606; Ig_Like.
PFam; PF00047; ig; 3.
PROST: SMO0407; ig: 1.
SWART; SMO0407; IGG1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                              Gaps
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
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HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.3%; Score 420; DB 1; Length 333; 69.8%; Pred. No. 5.1e-35; 1ve 19; Mismatches 13; Indels
                                                                              Length 290
                                                                                               Indels
S -> N (IN OMM).
/FTHG-VAR_003894.
MISSING (IN 2UC).
/FTIG-VAR_003895.
F -> Y (IN OMM).
/FTIG-VAR_003896.
W; E69CBC95705B2F46 CRC64;
                                                                                                                                                  64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                          181 QYNSTFRVVSALPIQHQDWASGKEFKCKVNNKALPSPIEKTISKPK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36497 MW; 55F8B64D48D460A6 CRC64;
                                                                            Score 504; DB 1; L, Pred. No. 1.6e-43; 9; Mismatches 5;
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01-FEB-1991 (Rel. 17, Last sequence update)
11-UL-1999 (Rel. 38, Last annotation update)
1g gamma-2B chain C region.
                                                                                                                                                                                                               333 AA
                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=89232738; PubMed=3149946;
                                                    290 AA; 32331 MW;
                                                                            86.7%;
                                                                           Query Match
Best Local Similarity 86.87
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.33
Best Local Similarity 69.83
Matches 74; Conservative
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                 227
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109
112
115
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333 AA;
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Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED GUINEA PIGS.
PIR, A02151; G2GP.
HSSP; P01772; ZEB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pig
the carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 4-68.
MEDLINE=71058471; PubMed=5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
Birshtein B.K., Hussain G.Z., Cebra j.J.;
"Structure of heavy chain from strain 13 quinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 134-226.
MEDLINE-7036072. PubMed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 227-311.
MEDLINE-7036073.
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
GC2_CAVPO STANDARD; PRT; 329 AA.

901862;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2 chain C region.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1975) to the PIR data bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 69-133 AND 312-329.
MEDLINE-71058486; PubMed=5538616;
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MEDLINE=71058474; PubMed=4922544;
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Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 13:4804-4811(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 3. SMART; SM00410; IG_like; 1. SMART; SM00407; IGcl; 2. PROSITE; PS00290; IG_MHC; 1.
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79
105
107
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202
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                                                                                                                                                                                                                                                                                                                                                                MEDINE-64030330; PubMed-6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                SEQUENCE OF 1-128.
MEDLINE-76135465; PubMed=1243651;
Pratt D.M., Mole L.E.,
"Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.",
Biochem. J. 151:337-349(1975).
                                                                                     2; Gaps
                                                                                                  2 PP---VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.; "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes."; Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- MISCELLANDOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKER.
                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit
                                                        71.8%; Score 417; DB 1; Length 329; 70.9%; Pred. No. 1e-34; Live 12; Mismatches 18; Indels
                                                                                                                                              60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                           178 N-LINKED (GLCNAC. . .)
308
3674 MW; 5D231B7164DIFBA9 CRC64;
                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                   323 AA
                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 88-266 FROM N.A.
MEDLINE=83299917; PubMed=6193512;
                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenetics 18:387-397(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tochem. J. 116:249-259(1970).
                                                                             Conservative
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                        gamma chain C region.
 178
248
329 AA;
                                                      Query Match
Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=85027161; PubMed=6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.M., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels
                                                                                                                                                                                                                                                                                                                                           T -> M (IN D11 MARKER).

T -> A (IN E15 MARKER).

V -> VPV (IN EEF 2).

V -> VPV (IN REF 2).

O -> E (IN REF 3 AND 4).

O -> E (IN REF 3 AND 5).

O -> E (IN REF 5).

E -> Q (IN REF 5).

E -> D (IN REF 5).

E -> D (IN REF 5).

E -> D (IN REF 5).

Y -> W (IN REF 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.1%; Score 413; DB 1; 69.1%; Pred. No. 2.5e-34;
                                                                                                                                                                                                                                                                                        domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region, secreted form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                           EMBL; M16426; AAA31289.1; -. PIR; A02161; GHRB.
                                                                                                             PIK; nvz....
HSSP; P01857; IFC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MM.
                                                                                                                                                                                                          Pfam; PF00047; ig; 3. ~SMART; SM00407; IGc1; 2. PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 69.19
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                       Pfam; PF00047; ig;
SMART; SM00407; IGC
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2 PP---VAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 58
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MEDINE-80012837, PubMed-113776;
ROGETS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-80202559; PubMed-6769752;
Obata M., Yamawaki-Rateoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDILINE-80045036; PubMed=115593; MEDILINE-80045036; PubMed=115593; Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                               Pfam; PF00047; ig; 3.
SWART; SW00410; IG_like; 1.
SWART; SW00407; IG_like; 1.
IMMART; SW00407; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                   E -> G (IN REF. 2).
E -> O (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.7%; Score 410.5; DB 1; 67.6%; Pred. No. 5.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 6:3305-3321(1979).
                                                                                                                                                                                                                                                                                    CH1.
HINGE.
CH2.
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MEDLINE=78242288; PubMed=98524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MΨ,
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
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                                                                                                                                                                                                                                                                                 97
1113
2223
3227
362
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333
342
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Cell 18:559-568(1979).
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Best Local Similarity
Thes 75; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 AA;
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P01868;
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                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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GG1_MODSE
GG1_MODSE
DT 21-JUL.
DT 30-MAY.
DE 19 gamm
RX MEDLINK
RX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PP----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wall R.; "The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-0CT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-3 Chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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SEQUENCE FROM N.A.
MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine 1963 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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SEQUENCE OF 328-398 FROM N.A.
SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                               PROSITE; PS00290; IC_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.7%; Score 410.5; DB 1; Length 329; Best Local Similarity 67.6%; Pred. No. 4.6e-34; Matches 75; Conservative 15; Mismatches 18; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||| |||||:|||| | : ||||: |||:||||| | 172 QPREAQYNSTERVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36228 MW; F45827174182BAD6 CRC64;
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                                                                                                                                                                                                                                                                                                        Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                              CH1.
HINGE.
CH2.
     EMBL; J00451; -; NOT_ANNOTATED_CDS PIR; B02156; G3MSC.
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ERML; VOL326; CAA24767.1; ALT_SEQ.
PIR; AQ1155; G3MSM.
HSSP; P01857; IFC1.
                                                           HSSP; P01857; 1FC1.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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223
327
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329 AA;
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P03987;
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DOMAIN
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GC3M_MOUSE
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Gaps

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18; Indels

Length 398;

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DOMAIN
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Adetugbo K.; "Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma gammal chain."; J. Biol. Chem. 253:6068-6075(1978).
                                                                                            "The disulphide bridges of a mouse immunoglobulin G1 protein."; Blochem. J. 126:837-850(1972).
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HEAVY CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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INTERCHAIN (WITH A H.
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INTERCHAIN (WITH A H.
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67.6%; Pred. No. 1.3e-3
***ive 19; Mismatches
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HINGE.
                                                            DISULFIDE BONDS (MOPC 21).
MEDLINE-7300889; PubMed-5073237;
Svasti J., Milstein C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                      EMBL; V00793; CAA24172.1; EMBL; V00793; CAA24172.1; EMBL; V00793; CAA24173.1; EMBL; V00793; CAA24175.1; EMBL; V00795; CAA24175.1; EMBL; V00795; CAA24176.1; PIR; A02159; GIMS.

GlycoSuiteDB; P01868; GlycoSuiteDB; P01868; InterPro; IPR003006; Ig_MHC. InterPro; IPR003006; Ig_C1.
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P01869;
21-JUL-1386 (Rel. 01, Created)
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                                                           DISULFIDE BONDS (MOPC
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                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing.
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324
276
278
324 AA;
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Best Local Similarity
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27
102
104
107
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DISULFID
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DISULFID
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CONFLICT
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DOMAIN
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GC1M_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamawaki-Kataoka Y. Nakai S., Miyata T., Honjo T.;

"Nucleotide sequences of gene segments encoding membrane domains of procedule sequences of gene segments encoding membrane domains of proc. Natl. Acad. Sci. U. S.A. 79:2633-2627(1982).

-I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJON SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEGMENT OF MU CHAINS. THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                    SEQUENCE OF 323-393 FROM N.A.
BEDLINE-82197626; PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
"mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00407; ĬĠcī; 2.
PROSTE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 323-366 FROM N.A.
MEDLINE=82115295; PubMed=6799207;
Meders J., Choi E., Souza L., Carter C., Word C.J., Kuehl Eisenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CH1.
HINGE.
CH2.
CH3.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
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SMART; SM00407; IGC
                                                                                                                                                                               NCBI_TaxID=10090;
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DOMAIN
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INTERCHAIN (WITH A LIGHT CHAIN).

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329 AA;
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Best Local Similarity
Matches 71; Conserv
                                                                            Query Match
Best Local Similarity
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15-JUL-1999
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GCAB_MOUSE
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                                                                                                                                                                                                                                                                                                    116 SVFIFPPRPKPKDVLTITLTPRVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88166903; PubMed-3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
"Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CH3. INTERCHAIN (WITH A LIGHT CHAIN).
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                                                                                                                                                                                                       Length 393;
                                                                                                                                                                                                                                              14; Indels
                                                                                                           POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4CC88343B7A1CE27 CRC64;
                                                                            N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                             68 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                       68.2%; Score 396; DB 1; 67.6%; Pred. No. 1.6e-32; iive 19; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 JUL-1999 (Rel. 38, Last annotation update)
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 AA
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HINGE.
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InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_c1.
InterPro: IPR003600; Ig_lke.
Pfam: PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE: PS00290; IG_MHC; 1.
                                                                                                                                                      Ψ.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                  43386
                                                                                                                                                                                                       Query Match
Best Local Similarity 67.68
Matches 69; Conservative
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340
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393 AA;
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HSSP; P0185
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P20762;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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"Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.; Multiple differences between the nucleic acid sequences of the 1gG2aa and IgG2aa and IgG2aa alleles of the mouse."; proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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                                                                                                                        Length 329
                                                                                                                                                                                 16; Indels
                               5FCD7B7933850773 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                   67 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                        Score 392; DB 1;
Pred. No. 3.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 AA
                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma-2A chain C region, B allele.
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MEDLINE-82037861; PubMed-6170065;
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307
36571 MW;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_1lke.
                                                                                                                     67.5%;
68.0%;
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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                                                                                                                                                                                 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-80081502; PubMed-117549; Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.; Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.; 2b immunoq1obulin heavy fanin."; Sequence 206:1303-1306(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-80120716; PubMed-6766534; Yamawaki Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.; Tamawaki Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.; Complete nucleotide sequence of immunoglobulin gamma2b chain gene of inmunoglobulin gamma2b chain gene Nature 283:786-789(1980).
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Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,

Kim H., Takahashi N., Kato K., Arata Y.;

"O-glycosylation in hinge region of mouse immunoglobulin G2b.";

J. Biol. Chem. 269:12346-12350(1994).

"PPM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH
MODIFIED WITH 2 SIALIC ACID RESIDUES.
PPVA-----GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
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                                                                                                            56 AKTRPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mouse immunoglobulin allotypes: post-duplication divergence of 2a and gamma 2b chain genes.";
Nature 296:761-763(1982).
                                                                                                                                       Immunoglobulin domain; Immunoglobulin C region; Glycoprotein. NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAINS
-!- MISCELLANBOUS: THE A ALLELE SEQUENCE IS SHOWN.
                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ig gamma-2B chain C region.
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MEDLINE=82173203; PubMed=6803173;
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SEQUENCE FROM N.A. (MPC 11).
MEDLINE-80081501; Pubmed-117548;
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HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfan; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
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P01866;
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REMOVED POST-TRANSLATIONALLY (PROBABLE).
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MEDLINE-82115295; PubMed-6799207;

ROGETS J., Chola E., Souza L., Carter C., Word C.J., Kuehl M.,

Elsenberg D., Wall R.;

"Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";

"Gene segments PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES PRECIES ENCODES MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3 END, ENCODED
IN SEPRATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
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MEDLINE-8222190; PubMed-6283537;
Yamawaki-Katekoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
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IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
-i- MISCELLANDOUS: THE A ALLELE SEQUENCE IS SHOWN.
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Pred. No. 3.4e-31;
'f. Mismatches 19; Indels
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T -> A (IN B ALLELE).
M -> D (IN B ALLELE).
L -> S (IN B ALLELE).
L -> S (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
K -> P (IN REF. 3 AND 3).
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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CC cr send an email to license@isb-sib.ch).

DR EMBL; J00462; AAB59659.1; ALT_INIT.

BR PIR; CO2154; CASMSW.

DR HSSP: P01857; IFC.

MCD: MGI:96462; AAB59659.1; ALT_INIT.

DR HSSP: P01857; IFC.

MCD: MGI:96462; AAB59659.1; ALT_INIT.

DR HSSP: P01857; IFC.

DR InterPro: IPR003006; Ig_MRC.

DR FARM: SW00407; Ig_al.

DR SWART: SW00407; Ig_al.

DR SWART: SW00407; IG_ALKe; 1.

DR SWART: SW00407; IG_ALKe; 1.

DR SWART: SW00407; IG_ALKe; 1.

DR PRESCRIPTION OF IG_ALKe; 1.
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126 GPSVFIFPPNIKDVLMISLTPRVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDY 185

6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQX 65

9 0 0

Query Match 65.7%; Score 382; DB 1; Length 405; Best Local Similarity 66.3%; Pred. No. 4.2e-31; Matches 69; Conservative 16; Mismatches 19; Indels

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Search completed: June 21, 2002, 09:00:23 Job time: 1447 sec

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Q96k68 homo sapien
Q96k08 homo sapien
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MEDLIN-21477448; Pubmed-11593034;

Hu Z., Garen A.;

"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";

Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

EMBL; AF272774; AAK58686.1;

"TOTHER, AP272774; AAK58686.1;
"TOTHER, AP272774; AAK58686.1;
"TOTHER, AP272774; AAK58686.1;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.4e-51;
2; Mismatches 3; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                      June 21, 2002, 08:32:21; Search time 176.89 Seconds (without alignments) 106.600 Million cell updates/sec
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Q95m34 equus cabal
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                                                                                                                                                                                                                       US-09-674-857-1
581
1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKAK 109
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099124 mus m
096814 mus m
099125 mus m
099131 mus m
099125 mus m
099125 mus m
099125 mus m
099126 homo s
096486 homo s
096646 homo s
096646 homo s
096646 homo s
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                               hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM protein - protein search, using sw model
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Q91LQ4
Q9DEQ4
Q9DEQ4
Q91Z05
Q99L35
Q99L35
Q99L25
Q9BCB0
Q9BCB0
Q9BCB0
Q9BCD0
Q9BCD0
Q9BCD0
Q9BCD0
Q9BCD0
                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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09D8W4
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sp_unclassified:*
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sp_mammal:*
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sp_phage:*
sp_plant:*
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sp_bacteriap:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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sp_virus:*
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396
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382
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Perfect
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-119(1998).
Immunobiology 199:105-119(1998).
INDML_REMBL; AJ300675; CAC44624.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of Cobnas encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its 11ght and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (MAY-11999) to the EMBL/GenBank/DDBJ databases.
ESBL; AFI23372; AAD40243.1;
"ISSP; P01842; 7PAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                        Lguus caballus (Horse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98383416; PubMed-9717671;
Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.2%; Score 443; DB 6; Length 337; 73.6%; Pred. No. 6.6e-41; Live 16; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                     Wagner B.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
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                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 2.
PR0SITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48142 MW;
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Best Local Similarity 73.00
Best Local Similarity 73.00
The Table 
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                        NCBI_TaxID=9796;
                                                                                                       (FRAGMENT).
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SEQUENCE
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                                                                                                            Gaps
                                                                                  8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1810060009RIK PROTEIN.
1GH-1 OR 1810060009RIK.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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        Length 437;
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                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.2%; Score 396; DB 11; Length 4 67.6%; Pred. No. 1.6e-35; live 19; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG_MHC; UNKNOWN_1.
51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                               68 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                14;
Query Match 68.2%; Score 396; DB 11;
Best Local Similarity 67.6%; Pred. No. 1.5e-35;
Matches 69; Conservative 19; Mismatches 14;
                                                                                                                                                                                                                                                                                                                             463 AA.
                                                                                                                                                                                                                                                                                                                             PRT;
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InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MIC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 3. 59-7.
SMART; SM00409; ig; 2.
SMART; SM00400; iG; 2.
SMART; SM00400; iGc; 1.
SMART; SM00410; iG_like; 1.
SMART; SM00410; iG_like; 1.
SMART; SM00410; iG_like; 1.
SEQUENCE 463 AA; 51007 WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 67.68
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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InterPro; IPR003597; Ig.
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RESULT
Q99L25
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Q99L31
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SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-PANCREAS;

RAMAIN-C57BL/6J; TISSUE-PANCREAS;

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Salto T., Rawanaka I.,

Rada K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H., Suzuki R., Tomita M., Wagner L., Washio T.,

Radi K., Okido T., Puruno M., Anio H., Badarelli R., Barsh G.,

Rakai K., Okido T., Puruno M., Anio H., Badarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Roustelli M.J., Bult C., Fletcher C., Fullia M., Mazzarelli J., Mombaerts P.,

Rotone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Whynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Norachizati.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PPVA-----GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metaria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                            56 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.7%; Score 382; DB 11; Length 473; Larity 62.3%; Pred. No. 5.7e-34; Conservative 17; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC010327; AAH10327.1; -- Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYPOTHETICAL 51.9 KDA PROTEIN.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                  HSSP; P01842; 7FAB.
MGD; MGI:96443; 1gh-1.
InterPro; 1PR003599; 1g-1.
InterPro; 1PR003509; 1g-1.
InterPro; 1PR003500; 1g-1ike.
InterPro; 1PR003506; 1g-1ike.
InterPro; 1PR003506; 1g-1ike.
InterPro; 1PR003506; 1g-1.
SMART; SM00407; 1g; 4.
SMART; SM00407; 1G; 2.
                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
EMBL; AK007918; BAB25349:1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 AA; 51946 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                          263 GPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                         6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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   Length 473;
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                                     19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interc.
Pfam; PF00047; 15, 2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
SMART; SM004109; IG_11ke; 1.
SMART; SM004109; IG_11ke; 1.

SMART; SM004109; IG_11ke; 1.

SMART; SM004109; IG_11ke; 1.

TGMC; DNNNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 DYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPK 361
                                                                                                                                                66 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.3%; Score 368; DB 11;
63.2%; Pred. No. 2e-32;
ive 18; Mismatches 21;
 Score 382; DB 11;
Pred. No. 5.7e-34;
                                                                                                                                                                                                                                                                         468 AA
                                     16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.7%;
                                     69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Conservative
                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01842; 7FAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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Q99L25;
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                                     Matches
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NCBI_TaxID=9606;
                                                                           Q9BQB8
                                 RESULT 10
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Q9BU10
                                                       09BQB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                               63.3%; Score 368; DB 11; Length 473; 63.2%; Pred. No. 2e-32; Live 18; Mismatches 21; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Strausberger R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
REMEL; BC004476; AAH04476.1; -.
RESP; PO1857; IG-1;
RICEPPO; IPR003597; Ig-c1.
RICEPPO; IPR003597; Ig-c1.
RICEPPO; IPR003606; Ig-like.
RICEPPO; IPR003006; Ig-MHC.
REMER; SM00407; IGc1; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00410; IG-like; 1.
SM PROSITE; SP600290; IG-MHC; UNKNOWN_3.
                                                                    | InterPro; | PR003599; | Iq. | InterPro; | IRR003599; | Iq. | InterPro; | IRR003509; | Iq. | InterPro; | IRR003500; | Iq. | InterPro; | IRR003006; | Iq. | InterPro; | IRR003006; | Iq. | InterPro; | IRR003006; | Iq. | Iq. | V. | InterPro; | IRR00407; | Iq. | Iq. | V. | Iq. | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.8%; Score 138; DB 4; Length 375; 28.7%; Pred. No. 4.6e-07; ive 25; Mismatches 45; Indels
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: RC003888: AAH03888.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 375 AA; 41314 MW; BIAOA0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BSZ1;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 41.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       67; Conservative
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Best Local Similarity 28.7%
Matches 29, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-LYMPH, LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q9BSZ1
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9 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 68
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                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                   C TISSUE—IXMPHOMA;
A Strausberg R.;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006180; ARH06180.1; -.
EMBL; BC001872; ARH01872.1; -.
R HSSP; PO1825; 7FAB.
InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003060; Ig_like.
R InterPro; IPR003060; Ig_like.
R InterPro; IPR003060; Ig_like.
R InterPro; IPR00409; IG. 2.
R SMART; SM00409; IG. 2.
SMART; SM00409; IG. 162.1; 4.
SMART; SM00406; IG. 116.2; 1.
RR SMART; SM00406; IG_like; 1.
RR SMART; SM00410; IG_like; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45; Indels
                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUB-LYMPH, LYMPHOMA;
Strauberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1; -.
HSSP; P01825; 7FAB.
InterPro; IPR003599; Ig.
              OFBORS,
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-070-2001 (TrEMBLrel. 17, Created)
01-070-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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23.8%; Score 138; DB 4;
Best Local Similarity 28.7%; Pred. No. 8.1e-07;
Matches 29; Conservative 25; Mismatches 45.
    597 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597
PRT;
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PRELIMINARY;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-RHABDOMYOSARCOMA;
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                       096GA6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                    9 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 68
                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 55.0 ND PROTEIN.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          096EY0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:20337).
Enden saplans (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                             5
                                                                                                                                                                      Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.8%; Score 138; DB 4; Length 597; 28.7%; Pred. No. 8.1e-07; Live 25; Mismatches 45; Indels
InterPro; IPR003597; Ig_c1.
InterPro; IPR003606; Ig_like.
InterPro; IPR003606; Ig_MC.
InterPro; IPR0030596; Ig_w.
InterPro; IPR003596; Ig_w.
Pfam; PF00047; Ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
SMART; SM0040; IG_MHC; UNKNOWN_3.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 597 AA; 65274 MW; 2DAFABFB7E055851 CRC64;
                                                                                                                                                                                            45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) . .
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                   69 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                69 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                   Query Match 23.8%; Score 138; DB 4; Best Local Similarity 28.7%; Pred. No. 8.1e-07; Matches 29; Conservative 25; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                      597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
TISSUE=PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.8
Best Local Similarity 28.7
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Q96EY0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN (PROTEIN FOR MGC:15420).

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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7
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                                                                                                                                                                                                                ; Score 138; DB 4; Length 613;
; Pred. No. 8.4e-07;
25; Mismatches 45; Indels
L1
SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AM111857.1; - 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001): -.
EMBL; BC009851; AAH09851.1; -.
SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 67.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | :: || :: || |: | 422 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | :: || :| || :| || 421 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK 461
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TISSUE-PRIMARY B-CELLS FROM TONSILS;
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28.7%;
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TISSUE-LYMPH, AND LYMPHOMA;
Strausberg R.;
                                                                                                                                                                                                     Query Match
Best Local Similarity 28.7%
watches 29; Conservative
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Best Local Similarity 28.7%
Matches 29; Conservative
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Search completed: June 21, 2002, 08:59:29 Job time: 1628 sec

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Fri Jun 21 09:21:04 2002
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

June 21, 2002, 08:30:46; Search time 224.82 Seconds (without alignments) 53.852 Million cell updates/sec Run on:

US-09-674-857-1 Perfect score:

581 1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKAK 109 Sequence:

Scoring table:

747574 segs, 111073796 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

747574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

4: /SIDSI/gcgdata/hold-geneseqy-geneaty-general-general-geneseqy-geneseqp-embl/AA1981.DAT:\*
5: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1981.DAT:\*
6: /SIDSI/gcgdata/hold-geneseqy-embl/AA1985.DAT:\*
7: /SIDSI/gcgdata/hold-geneseqy-embl/AA1986.DAT:\*
8: /SIDSI/gcgdata/hold-geneseqy-embl/AA1986.DAT:\*
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9: /SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:\*
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18: /SIDSI/gcgdata/hold-geneseqy-embl/AA1996.DAT:\*
19: /SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:\*
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27: /SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:\*
28: /SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:\*
28: /SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:\*
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20: /SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AA1999.DAT:\*
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22: /SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AA1999.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:\* A\_Geneseq\_032802:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:\*

#### SUMMARIES

|        | Description | Mutated CH2 sequen | 2A2 (Chimeric) hum | 2A2 (Chimeric) hum | 3F4 (Chimeric) hum | 3F4 (Chimeric) hum | Mutated CH2 sequen | Undefined ORF2 enc | Mutated CH2 sequen | Amino acid sequenc | Human IqG2. Homo | Human IgG2 Fc regi |  |
|--------|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|--|
|        | ar<br>T     | AAY54996           | AAW14933           | AAW14934           | AAW14939           | AAW14940           | AAY54998           | AAR41709           | AAY54997           | AAB07476           | AAB67203         | AAB76423           |  |
|        |             | 21                 | 18                 | 18                 | 18                 | 18                 | 21                 | 14                 | 21                 | 21                 | 22               | 22                 |  |
| Query  | Length      | 109                | 462                | 462                | 463                | 463                | 110                | 109                | 109                | 217                | 217              | 217                |  |
| Query  | Match       | 100.0              | 97.2               | 97.2               | 97.2               | 97.2               | 96.3               | 95.4               | 95.4               | 95.4               | 95.4             | 95.4               |  |
|        | score       | 581                | 265                | 565                | 565                | 565                | 559.5              | 554                | 554                | 554                | 554              | 554                |  |
| Result | . ON .      | 1                  | 7                  | 3                  | 4                  | S                  | 9                  | 7                  | 8                  | 6                  | 10               | 11                 |  |
|        |             |                    |                    |                    |                    |                    |                    |                    |                    |                    |                  |                    |  |

| Human immunoglobul<br>Human IL-2/Ig fusi | CD4-gamma2 chimeri<br>CD4-qamma 2 chimer | 9        | Human CD4-gamma2 c | ~        | m        | Human IgG2 chain C | The heavy chain of | Humanised 323/A3 ( | Human immunoglobul | The heavy chain of |          | The heavy chain of | heavy    | heavy    | heavy    | CD4-IgG2 chimeric | CD4-IgG2 chimeric | Human CD4-IgG2 chi | CD4-IgG2 chimeric | Heavy chain of ful | Human IgG2 huH52 h | CD4-IgG2 chimeric | pH52-8.0 humanised | The heavy chain of | D9D10 heavy chain | MoTAbII fusion pro |          | man      | sedn     | IL-20RA-Ig gammal | 0        |
|------------------------------------------|------------------------------------------|----------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|----------|----------|----------|-------------------|-------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|----------|----------|----------|-------------------|----------|
| AAE02643<br>AAY06895                     | AAR26782<br>AAR46678                     | AAY85079 | AAB80883           | AAB67322 | AAB72230 | AAY31670           | AAY93734           | AAB72236           | AAB26884           | AAY93701           | AAY93707 | AAY93727           | AAY93732 | AAY93703 | AAY93730 | AAR26783          | AAY85080          | AAB80884           | AAB67323          | AAW34505           | AAY08755           | AAR46679          | AAR30775           | AAY93728           | AAW85689          | AAW85692           | AAY05688 | AAW97756 | AAB07541 |                   | AAU04062 |
| 505                                      | 13                                       | 21       | 22                 | 22       | 22       | 20                 | 21                 | 22                 | 21                 | 21                 | 21       | 21                 | 21       | 21       | 21       | 13                | 21                | 22                 | 22                | 18                 | 20                 | 15                | 14                 | 21                 | 20                | 20                 | 20       | 20       | 21       | 22                | 22       |
| 326                                      | 432                                      | 432      | 432                | 432      | 442      | 443                | 451                | 461                | 462                | 463                | 463      | 463                | 463      | 464      | 464      | 530               | 530               | 530                | 530               | 450                | 450                | 530               | 552                | 463                | 468               | 711                | 251      | 251      | 251      | 559               | 594      |
| 95.4                                     | 95.4<br>95.4                             | 2        | 95.4               | 95.4     | 95.4     | 95.4               | S                  | 95.4               | 95.4               | 95.4               | 95.4     | 95.4               | S        | 95.4     | 95.4     | 95.4              | 95.4              | 95.4               | 'n                | 4.                 | 4                  | 4                 | ٠.                 | 4                  | 4                 | 4                  | 94.2     | 94.2     | 4.       | 94.2              | 94.2     |
| 554                                      | 554<br>554                               | 554      | 554                | 554      | 554      | 554                | 554                | 554                | 554                | 554                | 554      | 554                | 554      | 554      | 554      | 554               | 554               | 554                | 554               | 551                | 551                | 551               | 551                | 548                | 548               |                    |          |          |          | 547.5             | 547.5    |
| 13                                       | 14<br>15                                 | 16       | 17                 | 18       | 19       | 20                 | 21                 | 22                 | 23                 | 24                 | 25       | 26                 | 27       | 28       | 29       | 30                | 31                | 32                 | 33                | 34                 | 35                 | 36                | 37                 | 38                 | 36                | 40                 | 41       | 42       | 43       | 44                | 45       |

### ALIGNMENTS

AAY54996 standard; protein; 109 AA. Mutated CH2 sequence Gldeltaab. (first entry) 17-FEB-2000 AAY54996; AAY54996 RESULT 

Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human: immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-va-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaenia; Goodpastures disease; therapy; sickle cell anaemia; coronary artery occlusion.

Synthetic.

W09958572-A1

18-NOV-1999.

99WO-GB01441. 07-MAY-1999; 98GB-0009951. 08-MAY-1998;

(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

Clark MR, Williamson LM; Armour KL, Rollins S;

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A chimeric antibody (AAW14933) comprises the Cl and hinge regions of human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAD) and a murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (MAD) 2A2 heavy chain variable region sequence (see also AAW14932). The chimeric antibody is specific for porcine VCAM. It is useful for diagnosing human rejection of porcine central and for improving xenotransplants and for improving xenotransplantation of porcine cells, tissues and organs into human recipients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                        Antibodies binding to porcine but not human cell interaction proteins - useful to treat and assay for rejection of xenografted porcine organs, tissues or cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 565; DB 18;
Pred. No. 4.8e-50;
                                                                                                                                                                        Matis LA, Mueller EE, Mueller JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mueller JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2A2 (Chimeric) human G2/G4 chimeric antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 42-44; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chimeric antibody; diagnosis.
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97.2%;
   96US-0004489.
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                                                                                                     (ALEX-) ALEXION PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                      WPI; 1997-212855/19.
N-PSDB; AAT62931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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   26-SEP-1996;
28-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9711971-A1
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                                                                                                                                                                    Evans MJ,
Rother RP;
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                                                                                                                                                                                                                                                 This sequence represents the mutated CH2 molecule Gldeltaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target complement comprises: (a) a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant domain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FegammaRIID catabilition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule (a) an antibody, to the target colleding inhibitation of B cell activation, be used to prevent or inhibit binding of a second binding molecule, e.g. an antibody, to the target colleding and activation in the treatment of inhibit the binding molecule is useful for the treatment of graft-vs-host disease, organ transplant rejection, bone-marrow transplant rejection, autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. foetal/neonatal alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN cornary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through Fegamma and cornary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through Fegamma and allergy with behing able to cross the human placenta through interaction with FCRN which is consistent
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                                                           Immunoglobulin-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties -
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vascular cell adhesion molecule; VCAM; monoclonal antibody;
chimeric antibody; diagnosis.
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                                                                                                                                                                                                Claim 12; Fig 17; 81pp; English
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Matches 109; Conservative
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WPI; 2000-039075/03.
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Rother RP;
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                                         Antibodies binding to porcine but not human cell interaction proteins - useful to treat and assay for rejection of xenografted
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                                                                                Disclosure; Page 44-47; 105pp; English.
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                                                              porcine organs, tissues or cells
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97.2%;
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Best Local Similarity 97.2
Matches 106; Conservative
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Jot: 1997-212855/19.
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N-PSDB; AAT62936.
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                         N-PSDB; AAT62932
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Chimeric Mus sp.
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Rother RP;
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A chimeric antibody (AAW14939) comprises the Cl and hinge regions of human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAD) and a murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (MAD) 3F4 heavy chain variable region sequence (see also AAW14938). The chimeric antibody is specific for porcine VCAM. It is useful for diagnosing human rejection of porcine centransplants and for improving xenotransplants and organs into human recipients.
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Pred. No. 4.8e-50;
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Best Local Similarity 97.2%;
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding molecule of the invention. The recombinant binding molecule of the invention. The recombinant binding molecule of binding a target molecule without triggering complement dependent lysis, or the call-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and domain of a human inamunosjlobulin (GigG) heavy chain. The binding molecule is used to bind a target molecule (especially FogammaRIE) causing inhibition of B cell activation, mast cell degranulation or binding molecule can be used to prevent or inhibit the binding of a second binding molecule. Gig an antibody, to the target molecule. The binding molecule is useful for the treatment of graft-vs_host disease, organ transplant rejection, bone-marrow transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell-mediated destruction; human; immunoglobulin G; 1gG heavy chain; croph's disease; draft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; autoimmune disease; asthma; allergy; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; entitle alloimmune thrombocytopaenia; goodpastures disease; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb;
                                                                                                                       Gaps
                                                                                                                                                                       This sequence represents the mutated CH2 molecule Gldeltaac, and is a
                                                                                                                                                   1 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties -
                                                                                                                         .;
0
                                                                                        Length 463;
                                                                                                                                                                                                                   61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                        Indels
                                                                                                                       1;
                                                                                    Score 565; DB 18;
Pred. No. 4.8e-50;
2; Mismatches 1;
cells, tissues and organs into human recipients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sickle cell anaemia; coronary artery occlusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Armour KL, Clark MR, Williamson LM;
                                                                                                                                                                                                                                                                                                                                     AAY54998 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Fig 17; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutated CH2 sequence Gldeltaac.
                                                                                  97.2%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-GB01441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0009951
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                    Best Local Similarity 97.2
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-039075/03.
                                   463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9958572-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J7-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                        AAY54998;
                                                                                    Query Match
                                                                                                                                                                                                                                                    308
                                                                                                                                                                                                                                                                                                                       AAY 54998
                                                                                                                                                                                                                                                                                                       RESULT
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1;
rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia and arthritis), alloimmunity (e.g. foetal/neonatal alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN (erythroblastosis foetalis), Goodpastures, sickle cell anaemia and coronary artery orclusion). The binding molecules do not activate complement or trigger cytotoxic activities through FogammaR and desirable 1gG properties have been retained. The polypeptides do not contain non-human amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind protein A, which is consistent with being able to cross the human placenta through interaction with FCRn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma isotype, gamma-2, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy: light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVA-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21; Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 559.5; 98.2%; Pred. No. 3.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Undefined ORF2 encoded by plasmid pAH4625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 17J; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR41709 standard; Protein; 109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-US10206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                              (neonatal Fc receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ALKE-) ALKERMES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-196742/24.
N-PSDB; AAQ43846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR41709;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
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in which the heavy chain (VH) is derived from a murine source and the sequences encoding CH1. CH2 and CH3 are derived from a human source. This vector, in combination with the chimmeric light chain vector, pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated "18.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial colls. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods.
                                           8 \times 6666666666668 \times 8
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109 AA; Sequence

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0
                              Gaps
                                                      1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                    ő
Score 554; DB 14; Length 109;
Pred. No. 1.1e-49;
5; Mismatches 2; Indels
                                                                                                           61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                           95.4%;
93.6%;
Query Match 95.4
Best Local Similarity 93.6
Matches 102; Conservative
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Ŕ AAY54997 standard; protein; 109 Mutated CH2 sequence G2deltaa. (first entry) 17-FEB-2000 AAY54997; œ AAY54997 ID AAY5 

Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-va-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaenia; Goodpastures disease; sickle cell anaemia; coronary artery occlusion.

Synthetic.

18-NOV-1999

W09958572-A1.

99WO-GB01441. 07-MAY-1999; 98GB-0009951. 08-MAY-1998; (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

Williamson LM Armour KL, Clark MR,

WPI; 2000-039075/03.

complement or trigger cytotoxic activities and maintaining desirable Immunoglobulin-derived binding molecules that do not activate immunoglobulin properties -

Claim 12; Fig 17; 81pp; English.

This sequence represents the mutated CH2 molecule G2deltaa, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement

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dependent lysis, or the cell-mediated destruction of the target

comprises: (a) a binding domain capable of binding a target molecule;

comprises: (a) a binding domain capable of binding a target molecule;

comprises: (b) an effector domain that is homologous to all or part of a constant

consider the binding molecule (especially FegammaRID

considerable inhibition of B cell activation, mast cell degranulation or replayocytosis). The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the transplant consecute. The binding molecule is useful for the transplant rejection, autoimmunity (e.g. vasculitis, autoimmune haemolytic anaemia, activine autoimmune thrombocytopaenia and arthritis), alloimmunity

cautoimmune thrombocytopaenia and activities of consensation and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN

cartoimmune thrombocytopaenia, asthma and allergy), coronary artery occlusion). The binding molecules do not activate

complement or trigger cytotoxic activities through FegammaR and desirable consensement or trigger cytotoxic activities through regammaR and desirable immunogenicity. Further, they still bind protein A, which is consistent immunogenicity Further, they still bind protein A, which is consistent with being able to cross the human placenta through interaction with FCRn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Fc region-containing polypeptides that have altered effector function due to one or more amino acid modifications in the Fc region, useful in the treatment of cancer and allergic conditions such as asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IgG antibody; light chain; Fc region; effector function; cancer; allergy; asthma; LFA-1-mediated disorder; tumour; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.4%; Score 554; DB 21; Length 109; 94.5%; Pred. No. 1.1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of native IgG Fc region humIgG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB07476 standard; protein; 217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-2000; 2000WO-US00973.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (neonatal
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AAB07476
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AAB76423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
            S S S S S S
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                                                                                                                                                                                                                                                                                                                                                δ
                                               AAB07474-78 represent native IgG Fc regions. The proteins are used to produce Fc region-containing polypeptides that have altered effector function as a consequence of one or more amino acid modifications in the Fc region. The variant polypeptides are useful for treating cancer, allergic conditions such as asthma (with an anti-IgE antibody), and LEA-1-mediated disorders. Where the polypeptide binds the HER2 and LEA-1-mediated disorders. Where the polypeptide binds the HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a benign or malignant tumour characterized by overexpression of the HER2 receptor. Such cancers include breast cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, pladder cancer, gastrointestinal cancer, pladder cancer, pladder cancer, olon cancer, coloncarcal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 appvagpsvílfppkpkdtlmisrtpevtcvvvdvshedpevgfnwyvdgvevhnaktkp 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion protein; immunoglobulin; multidimerization domain; liqand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a fusion protein, comprising a peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (Ib). The hybrid melecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 554; DB 21;
Pred. No. 2.6e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
Disclosure; Fig 22A; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB67203 standard; protein; 217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000; 2000WO-US18185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0142088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dennis MS, Lazarus RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-123106/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200102440-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB67203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides represented in AAB76350 - AAB76420 and AAB76432 - AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences used in the invention of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers. CC diseases of the nervous system musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia, cinfection, metabolic disorders, nutritional deficiency or toxic agents. CI nparticular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease con an one of the diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human
                                                                                                                                                                           Gaps
                                                                                                                                                                                                               1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                   2 appvagpsvílíppkpkdtlmisrtpevtcvvvdvshedpevqfnwyvdgvevhnaktkp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-naturally occurring peptide ligands which compete for binding erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
example the peptide ligand can bind ErbB2. The peptide ligand may bind to and inhibit the activity associated with a particular
                                                                                                                                                                           ö
                                                                                                                                  Length 217;
                                                                                                                                                                                                                                                                                                          61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                           Indels
                                                                                                                                  Score 554; DB 22;
Pred. No. 2.6e-49;
5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 1962 Fc region amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Figure 2A; 116pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAB76423 standard; Protein; 217
                                                                                                                                    95.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000, 2000WO-US18283.
                                                                                                                                                       93.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-123048/13.
                                                                                                                                                       Local Similarity
Les 102; Conserv
                                                                          217 AA;
                                        target molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dennis MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB76423;
                                                                            Sequence
                                                                                                                                    Query Match
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Matches
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Gaps

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Matches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                    AAY06895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gillies S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel modified erythropoletin forms such as fusion proteins, comprisir Fc portion of an immunoglobulin molecule and a target molecule having the biological activity of erythropoietin forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, erythropoietin, EPO; antianaemic; nephrotrophic; anti-HIV;
vaccine; haemostatic; immunoglobulin G2; IgG2; EPO deficient disease;
anaemia; renal failure; Human Immunodeficiency Virus; HIV;
                                                                                                                                                Gaps
                                                                                                                                                                                                  1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                             2 appvagpsvílfppkpkdtlmisrtpevtcvvvdvshedpevgfnwyvdgvevhnaktkp 61
                                                                                                                                                ö
                                                                                        Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Way JC,
                                                                                                                                                                                                                                                                                                                                    61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunoglobulin G2 constant region mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ×
                                                                                                                                                ;
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                                                                                        95.4%; Score 554; DB 22; 93.6%; Pred. No. 2.6e-49;
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                                                                                                                                                5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 24; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ωì
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE02643 standard; Protein; 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rieke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haematopoietic growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-2000; 2000WO-EP10843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERE ) MERCK PATENT GMBH.
                                                                                                                                             Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brandt S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-367563/38.
                                                                                                                    Similarity
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             217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE02643;
Seque
                                                                                           Query Match
                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE02643
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The invention relates to vaccine compositions comprising a vaccine and a timed release formulation of a cytokine or cytokines/immunoglobulin fusion protein or plasmid at one or more temporal points subsequent to vaccine administration. The vaccines can be used for treating an autoimmune disease, an infectious disease, an inflammatory disease, a neoplastic disease, or an immunologic disease in an individual. The vaccines can be used to elicit immune responses against diseases such as AIDS, malaria, tuberculosis, hepatitis C, hepatitis B, cancer or influenza. The methods an antibody response, a cellular proliferative response as well as an antibody response, a cellular proliferative response as well as cytotoxic T-lymphocyte levels. In addition the Ig can increase the circulating half life of the cytokine. The present sequence represents a human interleukin-2 (IL-2)/Ig fusion protein.
                                                                                                                                                                                                                                                                                                   Fusion protein; vaccine; cytokine; immunoglobulin; autoimmune disease; infectious disease; inflammatory disease; neoplastic disease; cancer; immunologic disease; immune response; malaria; tuberculosis; hepatitis; AIDS; influenza; interleukin; II-2; Ig; human.
              1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                        REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                        (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Fig 10A-E; 66pp; English.
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                                                                                                                                                                          AAY06895 standard; Protein; 381
                                                                                                                                                                                                                                                                     Human IL-2/Ig fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US20321,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0990180.
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vaccine compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barouch DH, Letvin NL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-254931/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX34598
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                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1997;
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Length 381;

DB 20;

95.4%; Score 554;

Query Match

Length 326;

Score 554; DB 22; Pred. No. 4.3e-49;

95.4%;

Query Match Best Local Similarity

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Gaps

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Indels

No. 6.1e-49; smatches 2;

Pred. No. 6.1e 5; Mismatches

93.68;

Best Local Similarity

102;

Matches

οy

Conservative

1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Try was produced by expression of the coding mutagenised cDNA (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV of heavy chain dimers. It can inhibit HIV infection of CD4 cells and block the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, ego biphtheria, peeudomnas exotoxin A (domains I or II) or the deglycosylated A-chain
                                                         Gaps
                                         1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a CD4-gamma2 chimeric heavy chain homodimer.
                                                                                                                                                                                                                                                                                                      soluble CD4; T cell receptor; CD4 antigen; high recovery; increased serum half life; HIV infection; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for treatment, prevention and diagnosis of HIV infection
                                                                                                             REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                 Indels
               ..
  Pred. No. 5.2e-49;
5; Mismatches 2
                                                                                                                                                                                                                                                                          CD4-gamma2 chimeric heavy chain homodimer
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                           AAR26782 standard; Protein; 432 AA.
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93.68;
                                                                                                                                                                                                                                                                                                                                                                                                                217..325
/label= CH2
326..433
/label= CH3
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/label= CD4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROG-) PROGENICS PHARM INC.
                                                                                                                                                                                                                                                 (first entry)
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beaudry GA, Maddon PJ;
                                                                                                                                                                                                                                                                                                                                               Homo sapiens chimeric.
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N-PSDB; AAQ28088.
 Similarity
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A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected subjects to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate comprising the radionuclide can be used to image HIV efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject.
                                                                                                                                                                                                                            CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV; human immunodeficiency virus; radionuclide; toxin; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-1gG2 immuno:conjugates - used to kill HIV-infected cells and to image and stage HIV infection
                                               61 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                        treatment; imaging; detection; targetting.
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217 305
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/label= CH2 Region.
326..432
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205..216
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N-PSDB; AAQ57750.
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Search completed: June 21, 2002, 08:36:04 Job time: 318 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Run on:

June 21, 2002, 09:00:23 ; Search time 48.19 Seconds (without alignments) 87.579 Million cell updates/sec

US-09-674-857-2 580 1 APPVAGPSVFLFPPKFKDTL.......CKVSNKGLPSSIEKTISKTK 109

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|           | Description  | P01859 homo sapien | homo      | рошо      | рошо      | 2 cavia   | _       | P01870 oryctolagus |           | 7          | P01868 mus musculu | P01869 mus musculu | P20762 rattus norv | P20759 rattus norv | P01864 mus musculu | P01866 mus musculu | шns        | P01863 mus musculu | P01865 mus musculu | P20760 rattus norv | P01854 homo sapien | P20768 suncus muri | P01855 rattus norv | mus n     | P04220 homo sapien | 1 homo    | _         | P01834 homo sapien | P06337 mesocricetu | P01872 mus musculu | m          | P20763 gallus gall | P01874 canis famil | P01877 homo sapien |
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| COLUMNIA  | ID           | GC2_HUMAN          | GC4_HUMAN | GC1_HUMAN | GC3_HUMAN | GC2_CAVPO | GCB_RAT | GC_RABIT           | GC3_MOUSE | GC3M_MOUSE | GC1_MOUSE          | GCIM_MOUSE         | GCC_RAT            | GC1_RAT            | GCAB_MOUSE         | GCB_MOUSE          | GCBM_MOUSE | GCAA_MOUSE         | GCAM_MOUSE         | GCA_RAT            | EPC_HUMAN          | MUC_SUNMU          | EPC_RAT            | EPC_MOUSE | MUCB_HUMAN         | MUC_HUMAN | ALC_RABIT | KAC_HUMAN          | MUC_MESAU          | MUC_MOUSE          | MUCM_MOUSE | LAC_CHICK          | MUC_CANFA          | ALC2_HUMAN         |
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|           | Watch Length | 326                | 327       | 330       | 290       | 329       | 333     | 323                | 329       | 398        | 324                | 393                | 329                | 326                | 335                | 336                | 405        | 330                | 399                | 322                | 428                | 457                | 429                | 421       | 391                | 454       | 299       | 106                | 454                | 455                | 476        | 103                | 450                | 340                |
| ж<br>(    | Match        | 98.6               | 92.4      | 90.3      | 89.0      | 73.3      | 72.9    |                    |           | 70.8       | ٠                  | 70.7               |                    |                    | 96.0               |                    | 0.99       |                    | 65.2               |                    | 29.7               | 26.2               |                    | 25.2      | 4                  | 24.1      | ω.        | ж                  | 23.1               | m                  |            | 22.1               | 22.0               | 21.3               |
|           | Score        | 572                | 536       | 524       | 216       | 425       | 423     | 418                | 410.5     | 410.5      | 410                | 410                | 400                | 384                | 383                | 383                | 383        | 378                | 378                | 342                | 172.5              | 152                | 147                | 146       | 141                | 140       | 136.5     | 135                | 134                | 134                | 134        | 128                | 127.5              | 123.5              |
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| P20758 gorilla gor<br>P01876 homo sapien<br>P01898 oryctolagus<br>P04221 oryctolagus<br>P01843 mus musculu<br>P01843 homo sapien<br>P20765 mus spretus<br>P20764 mus musculu<br>P23084 heterodontu<br>P15814 homo sapien<br>P15814 mos sapien<br>P01848 mus musculu |
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| ALC1_GORGO ALC1_HUMAN MUC_RABIT MUCM_RABIT IAC1_MOUSE IAC2_HUMAN IAC5_MOUSE IAC5_MOUSE ILAC5_HUMAN ILAC4_RABIT ALC_MOUSE                                                                                                                                            |
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## ALIGNMENTS

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                                                                                                                                                                                                                 MEDLINE-95255298; PubMed-7737190; Stoppini G., Garver F., Ferri G.; "Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                DISULFIDE BONDS.
MEDLINE-72033500; PubMed-4940472;
Milstein C., Frangione B.;
"Disulphide bridges of the heavy chain of human immunoglobulin G2.";
Biochem. J. 121:217-225(1971).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-69064124; PubMed-5782707; Frangione B., Milstein C., Pink J.R.L.; "Structural studies of immunoglobulin G."; Nature 221:145-148(1969).
                                                                                REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
                                                                                                                                    Submitted (MAR-1980) to the PIR data bank
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HINGE.
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immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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InterPro; IPR003600; Ig_like.
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HSSP; P01857; 1FC1.
MIM; 147110; -
InterPro; IPR003006; Ig_MHC.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGCl; 2.
PROSITE; PS00290; IG_MHC; 2.
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    Score 572; DB 1; Length 326; Pred. No. 4.7e-51;
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1; Indels
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98.2%;
Ouery Match
Best Local Similarity 98.2°
Matches 107; Conservative
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0; Gaps Score 536; DB 1; Length 32. Pred. No. 2.2e-47; 3; Mismatches Query Match
Best Local Similarity 94.3\*
Matches 100; Conservative

4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63

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MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
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                                                                                                                                                                                                                                                                    MEDLINE-82274238; PubMed-6287432;
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Nucleic Acids Res. 10:4071-4079(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgGl KOL, I.";
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE (MYELOMA PROTEIN NIE).

MEDLINE-7707059; PubMed-826475;

Ponstingl H., Hilschmann N.;

"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-71064027; PubMed-4923144;
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-71064025; Pubmed-5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
                                               QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                    330 AA
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MEDLINE-77070267; PubMed-1002129;
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                                                                                                      "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";

Biochemistry 20:2361-2370 (1981).

-I- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 299-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.

-I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

-I- MISCELLANEOUS: BOTHERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                    -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_c1.
InterPro: IPR0035600; Ig_like.
InterPro: IPR003600; Ig_like.
InterPro: IPR003600; Ig_like.
SMART; SMO0410; IG_like; 1.
SMART; SMO0407; IG_like; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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/FIId-VAR_003886.

D -> E (IN GIM(NON-1) MARKER).

/FIId-VAR_003887.

L -> M (IN GIM(NON-1) MARKER).

/FIId-VAR_003888.
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INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
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REMOVED POST-TRANSLATIONALLY.
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                                                                      MEDLINE-81208100; PubMed-7236608;
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PDB; 1FC1; 15-JUL-92.
PDB; 1FC2; 15-JUL-92.
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MEDLINE-81021548; PubMed-6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
Prinary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-77118561; PubMed-402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1g-amma-3 chain C region (Heavy chain disease protein) (HDC). IGHG3.
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MEDIINE-77021516; PUDMEd-823945;
WOlfenstein-Todel C., Frangione B., Prelli F., Franklin B.C.;
With a maino acid sequence of 'heavy chain disease' protein zUC.
Structure of the Fc fragment of immunoglobulin G3.";
Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                         Length 330;
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                                                                                                                                                                                                                                                                                                                       36106 MW; 3770EE106C2FA33D CRC64;
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Pred. No. 3.6e-46;
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86.0%;
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                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CH1 REGION.
-!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.
-!- MISCELLANEOUS: DISEASE PROTEIN OWM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.
-!- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
                                                                                       Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE RESION.

-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.

-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
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INTERCHAIN (WITH HEAVY CHAIN DIMER).

             Franklin E.C., Hood L., Buxbaum J.N.; "Gamma Heavy chain disease in man: CDNA sequence supports partial gene deletion model.";
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Alexander A., Steinmetz M., Barritault D., Frangione B.,
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P > L (IN OWM).
/FTId=VAR_003891.
F > Y (IN OWM).
/FTId=VAR_003892.
T -> A (IN OWM).
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HSSP; P01857; IFC1.
MIM; 147120; ...
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003500; Ig_Like.
Ffam; PF00047; ig; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 1.
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Biochemistry 10:26-31(1971).
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"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74.473-482(1988).
PIR; PSO018: PSO018.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                               PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
NON_TER 1 1 1
DISULLED 16 16
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FUL-1999 (Rel. 38, Last annotation update)
15-gamma-2B chain C region.
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MEDLINE-89232738; PubMed-3149946;
                                                                                                         HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
                                                   13 INBRED GUINEA PIGS.
PIR; A02151; G2GP.
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Matches 80; Conservative
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142
178
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329 AA;
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SEQUENCE
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P20761;
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the carboxyl-terminal
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MEDILINE-11058471; PubMed-5538606;

Birshtein B.K., Hussain Q.Z., Cebra J.J.;

Birshtein B.K., Hussain Q.Z., Cebra J.J.;

"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cystine joining heavy and light chains.";
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                   4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
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Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig gamma-2 chain C region.
Cavia porcellus (Guinea pig).
Cavia porcellus (Guinea pig).
Mammalia: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI_TaxID-10141;
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                                                                                                                                                                                                                               Length 290,
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                                           MISSIG (IN ZUC).
/FIId=VAR_003895.
F -> Y (IN OMM).
/FIId=VAR_003896.
W; E69CBC95705B2F46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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                                                                                                                                                                                                                       Query Match 89.0%; Score 516; DB 1; Best Local Similarity 89.6%; Pred. No. 2.1e-45; Matches 95; Conservative 7; Mismatches 4
S -> N (IN OMM).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 AA
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Submitted (APR-1975) to the PIR data bank.
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MEDLINE-71058486; PubMed-5538616;
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                                                                                                                                                    290 AA; 32331 MW;
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Best Local Similarity 70.08 Matches 77; Conservative
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SMART; SM00407; IGc1; 2.
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P22436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-76135469; PubMed-1243651; Pratt D.M., Mole L.E.; Mole L.E.; Mole L.E.; Adquence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype."; Blochem. J. 151:337-349(1975).
                                                                                                                      Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                        Gaps
                                                                                                         4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 88-266 FROM N.A.
MEDLINE-81399917: PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE-70110015; Pubmed-5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gamma globulins, Nobel Symp. 3, pp.109-127, Almqvist and Wiksell, Stockholm (1967).
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                                                               Length 333;
                                                            72.9%; Score 423; DB 1; Length 33 70.8%; Pred. No. 7.1e-36; Live 18; Mismatches 13; Indels
                                                                                                                                                      64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                      SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
                           55F8B64D48D460A6 CRC64;
                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma chain C region.
                                                                                                                                                                                                                                           323 AA
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                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=84030930; PubMed=6313520;
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           311
: 36497 MW;
                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
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                                                                       Best_Local Similarity 70.8%
Matches 75; Conservative
                                                                                                                                                                                                                                         STANDARD;
 147 2
253 3
333 AA;
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P01870;
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or send an email to license@isb-sib.ch).
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Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE-85627161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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IN REF. 2).
REF. 3 AND 4).
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69E8AA118D579A8B CRC64;
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-> A (IN E15 MARKER).
> E (IN REF. 2).
> VPV (IN ...
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Mus musculus (Mouse).
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Mammalia; Eutheria; Rodentia;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
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P01868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PP---VAGPSVFLFPPKPKDTLMISRTPEVICVVVDVSHEDPEVQFNWYVDGVEVHNAKT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-0CT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-3 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; Structural analysis of the murine 19G3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                       Pfam: PF00047; 19; 3.
SWART: SW00410; IG_like; 1.
SWART: SW00407; IG_like; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 329;
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                                                                                                                                                                                                                                                                97 CH1.
113 HINGE.
223 CH2.
327 CH3.
36228 MW; F45827174182BAD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             70.8%; Score 410.5; DB 1;
67.6%; Pred. No. 1.3e-34;
tive 15; Mismatches 18;
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                                                                                                                                                                                                                          Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
EMBL; 'J00451; -; NOT_ANNOTATED_CDS
PIR; B02156; G3MSC.
HSSP; P01857; IFC1.
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BML; V01256; CAA24767.1; ALT_SEQ.PIR; AQ2155; GBMSM.
HSSP; P01857; 1FC1.
                                              HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
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Best Local Similarity 67.68
Watches 75; Conservative
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P03987;
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SEQUENCE
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MEDLINE-80012837; PubMed-113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PP---VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKT 58
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MEDLINE=80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDILINE-80045036; Pubmed-115593; MEDILINE-80045036; Pubmed-115593; Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y., "Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                              PRGMI, PF00047; 19; 3.
SWART: SW00410; IG_like; 1.
SWART: SW00407; IG_like; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 KPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.8%; Score 410.5; DB 1; 67.6%; Pred. No. 1.6e-34;
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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CYTOPLASMIC
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Nucleic Acids Res. 6:3305-3321(1979)
                                                                                                                                                                             Transmembrane; Alternative splicing.
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HINGE.
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MEDLINE-78242288; Pubmed-98524;
                                                                                                                                                                                                                                                                                          CH3
                                                                                                                                                                                                                                                                                                                                                                                                                             MM:
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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Mus musculus (Mouse).
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Cell 18:559-568(1979).
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                                                                             DISJUFIDE BONDS (MOPC 21).
MEDLINE-73008B891; PubMed=5073237;
Svasti J., Milstein C.;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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                Evolution of immunoglobulin subclasses. Primary structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfan; PF00047; 19; 3.
SMART; SM00407; 16c1; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin Cregion; Glycoprotein; Alternative splicing.
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 410; DB 1;
Pred. No. 1.4e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 AA.
                                murine myeloma gammaī chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                  EMBL, V00793; CAA24172.1; --
EMBL, V00793; CAA24173.1; --
EMBL, V00793; CAA24173.1; --
EMBL, V00793; CAA24175.1; --
EMBL, V00795; CAA24175.1; --
PIR; A02159; GIMS.
HSSP, P01842; 7FB.
GlycosultedB; P01868; --
MGD; MGD; MG196446; IGHC.
InterPro; IPR003006; IG_MRC.
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P01869;
21-JUL-1986 (Rel. 01, Created)
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198
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276
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276
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324 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YERRADAR Y., NARAY S. M., MIYATA T., HONJO T.;
YERRADAR Y., NARAY S., MIYATA T., HONJO T.;
NUCLOCIDE SEQUENCES OF GENE SEGMENTS ENCODING MEMBRANE CALL SEG SEGMENTS.", 79:2623-2627(1982).

PLOC. NALL. ACAG. SCI. U.S.A. 79:2623-2627(1982).

-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. THE MAJOR SPECIES PRODUCES BENEBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE ? ENCOPED IN SEBARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O., "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 323-366 FROM N.A.
MEDLINE-82115295; PubMed-6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Elsenberg D., Wall R.,
"Gene segments encoding transmembrane carboxyl termini of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SMO407; ÍGc1; 2.
PROSTER; PSO0290; IC_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
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HINGE.
CH2.
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Cell 26:19-27(1981).
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
PIR; B021.9; GIMSM.
HSSP; P01842; 7FAB.
MGD; MGI: 96446; Igh-4.
InterPro; IPPR003006; Ig_MHC.
InterPro; IPPR003007; Ig_C1.
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Cell 18:559-568(1979).
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                                                                                                                                                                               Rátíus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                 Gaps
                                                                                                                                                                    8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.; Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3."; Eur. J. Immunol. 18:317-319(1988).
     HEAVY CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
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                                                                                                                         70.7%; Score 410; DB 1; Length 393; 71.6%; Pred. No. 1.8e-34;
                                                                                                                                              16; Mismatches 13; Indels
                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4CC88343B7AICE27 CRC64;
                                               N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                              68 TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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HSSP; P01857; 1FC1.
InterPro; IPR003060; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003507; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
FROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
19 gamma-2C chain C region.
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                                                        244
340
358
393 AA;
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"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74:473-482(1988).
PIR; PS0017; PS0017.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                        Length 329,
                                                                                                            16; Indels
                    SFCD7B7933850773 CRC64;
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013BAB45EF49B9DA CRC64;
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                                                                      ;; Score 400; DB 1;
;; Pred. No. 1.5e-33;
15; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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HINGE.
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MEDLINE-89232738; PubMed-3149946;
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219 CH
219 CH
82 CH
102 IN
106 IN
110 IN
111 IN
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3546 MW;
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36571 MW;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                        69.0%;
69.9%;
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                                                                      Query Match 69.0%
Best Local Similarity 69.9%
Matches 72; Conservative
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249
329 AA;
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140
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326 AA;
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Best Local Similarity
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musculus (Mouse)
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-82037777; PubMed-6794027;
Dogin M.J., Lawbereys M., Strosberg A.D.;
"Multiple amino acid Substitutions between murine gamma 2a heavy chain Fc regions of Igla and Iglb allotypic forms.";
Proc. Nall. Acad. Sci. U.S.A. 78 44031-40351(1981).
-!- MISCELLANBOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE, FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                          STRAIN-C57BL/6;
MEDLINE-82037861; PubMed-6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
"Multiple differences between the nucleic acid sequences of the IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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9
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Pred. No. 8.4e-32;
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                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2A chain C region, B allele.
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(Rel. 01, Last sequence update)
(Rel. 40, Last annotation update)
chain C region.
                      335 AA.
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                      PRT;
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PIR; A02153; G2MSAB.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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62.3%;
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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Matches 71; Conservative
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                                                                                                                                                                                                   NCBI_TaxID=10090;
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21-JUL-1986
16-OCT-2001
Ig gamma-2B
                  GCAB_MOUSE
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P01866;
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GCB_MOUSE
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MEDILINE=94216359; PubMed=7512967;

MEDILINE=94216359; PubMed=7512967;

Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,

Irimura T., Takahashi N., Kato K., Arata Y.;

"0-91ycosylation in hinge region of mouse immunoglobulin G2b.";

J. Biol. Chem. 269:12345-12350(1994).

"1- FTM. O-LINKED GIYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS

MODIFIED WITH 2 SIALIC ACID RESIDUES.

"INCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mouse immunoglobulin allotypes: post-duplication divergence of gamma 2a and gamma 2b chain genes.";
Nature 296:761-763(1982).
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                                                                                                                                                                                                                                                                                                                            Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.; "Structure of the constant and 3' untranslated regions of the murine gamma 2b heavy chain meseenger RNA."; Science 206:1299-1303(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.; "Sequence of the cloned gene for the constant region of murine gamma 2D immunoglobulin heavy chain."; Science 206:1303-1306(1979).
                                                                                                                                                  Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T., "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
                            Sciurognathi; Muridae; Murinae; Mus.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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NON TER

1 I I INTERCHAIN (WITH A LIGHT CHAIN)
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T -> A (IN B ALLELE).

M -> D (IN B ALLELE).

M -> I (IN B ALLELE).

L -> S (IN REF. 2 AND 3).

S -> P (IN REF. 2 AND 3).

T -> T (IN REF. 2 AND 3).

T -> T (IN REF. 2 AND 3).
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PIR; A02157; G2MS11.
HSSP; P01857; 1FC1.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003609; Ig_like.
FRAMRY: SM00447; IG_like; I.
SMART; SM00440; IG_like; I.
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                                                                                              SEQUENCE FROM N.A. (A ALLELE).
MEDLINE=80120716; PubMed=6766534;
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MEDLINE=82173203; PubMed=6803173;
Ollo R., Rougeon F.;
                                                                                                                                                                                                      cloned from newborn nouse DNA.";
Nature 283:786-789(1980).
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (MPC 11).
MEDLINE-80081501; Pubmed=117548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-80081502; Pubmed=117549;
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36
239
336 AA;
                                                    NCBI_TaxID=10090;
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0;
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Ouery Match 66.0%; Score 383; DB 1; Length 336; Best Local Similarity 66.3%; Pred. No. 8.4e-32; Matches 69; Conservative 16; Mismatches 19; Indels
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Og1v32 m adult mal
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Q99m11 mus musculu
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mus musculu
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EMBL, AF272774; AAK58686.1; SEQUENCE 701 AA; 77826 WW; 94AC6CEB42CC992F CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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86.0%; Pred. No. 3.9e-50;
iive 6; Mismatches 4; Indels
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09UP60
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091X92
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MEDLINE-21477448; PubMed-11593034;
Hu Z., Garen A.;
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Copyright (c) 1993 - 2000 Compugen Ltd
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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         Length 437;
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOM35; AAH03435.1; --
HSSP; P01842; 7FAB.
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                                                                                                                                                  289 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 330
                                                                                                                                  68 TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
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         70.7%; Score 410; DB 11; 71.6%; Pred. No. 1.3e-37; ive 16; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 AA.
                                                                                                                                                                                                                                          463 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF0004,; -y, -SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 2.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WH C.
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01-JUN-2001 (TrEMBLrel. 17, Ls
01-DEC-2001 (TrEMBLrel. 19, Ls
181006009RIK PROTEIN.
IGH-1 OR 1810060009RIK.
Mus musculus (Mouse).
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Matches 73; Conservative
                                         73; Conservative
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                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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            Query Match
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                                        Matches
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Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
Leibold W., Radbruch A.;
Gorganization of the equine immunoglobulin heavy chain constant region
genes III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBL_raxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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0
                                                                                                                                                                                                                                                                                                                                                                                                                           76.4%; Score 443; DB 6; Length 337; 73.6%; Pred. No. 1.9e-41; tive 17; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single chain antibody (scrv)..;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF152372; AAD40243.1;
EMSP. P01842; PTB.
InterPro; IPR003600; Ig_like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR00396; Ig_v.
FF00047; ig; 4.
SMART; SM00406; IGv.
SMART; SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wagner B.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48142 MW; 5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O.1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMAL HEAYY CHAIN OF MAB7 (FRAGMENT).
MUS MUSCUlus (Mouse).
           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMINGOBULIN GAWMA 1 HEAVY CHAIN CONSTANT REGION
(FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                        Equus caballus (Horse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE
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SEQUENCE
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Ra Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,
Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ra Cohrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ra Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Brownstein M.J., Bult C., Retcher C., Fujita M., Gariboldi M.,
Ra Brownstein M.J., Hull D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Nordone P., Ring B., Rilnqwald M., Rodriguez I., Sakamoto N.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ranki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Havachizaki V., Kawaji H., Kohtsuki S.,
Radota R., Kawai H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 AKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; AAH10327.1; -.
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MW; 9DED57A514475FBB CRC64;
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InterPro: IPR003599; 1g-1.
InterPro: IPR003599; 1g-2.
InterPro: IPR003600; 1g_1ke.
InterPro: IPR003006; 1g_NHC.
InterPro: IPR003006; 1g_NHC.
InterPro: IPR003596; Ig_NHC.
INTERPRO: IG_NHC
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SEQUENCE 473 AA; 51699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1;
HSSP; P01842; 7FAB.
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Best Local Similarity
Matches 71; Conserv
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SEQUENCE FROM N.A.
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Q91205;
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                      263 GPSVFIFPPNIKDVLAMISLIPKVICVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDY 322
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                ö
Length 473;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; interp
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1;
HSSP; P01842; 7FAB.
HCSP; P01842; 7FAB.
InterPro; IPR003599; 1g.cl.
InterPro; IPR003597; 1g.cl.
InterPro; IPR003500; 1g_like.
InterPro; IPR003506; 1g_like.
InterPro; IPR003506; 1g_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.2%; Score 369; DB 11;
63.2%; Pred. No. 5.5e-33;
live 18; Mismatches 21;
Query Match 66.0%; Score 383; DB 11; Best Local Similarity 66.3%; Pred. No. 1.5e-34; Matches 69; Conservative 16; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILAR TO RIKEN CDNA 1810060009 GENE.
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01-JUN-2001 (TrEWBLrel. 17, Created)
01-JUN-2001 (TrEWBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 63.28
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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PRELIMINARY;
                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                        NCBI_TaxID=9606;
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Q9BU10
              RESULT
                            09BQB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                   09BSZ1;
01-JUN-2001 (TEMBLrel. 17, Created)
01-JUN-2001 (TEMBLrel. 17, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
HYPOTHETICAL 41.3 KDA PROTEIN.
HOMO Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                             Query Match 63.6%; Score 369; DB 11; Length 473; Best Local Similarity 63.2%; Pred. No. 5.5e-33; Matches 67; Conservative 18; Mismatches 21; Indels (
     Submitted (FB 2001) to the EMBL/GenBank/DDBJ databases.

R BABL; BC003888; AAH03888.1; -. RBL; BC003888; AAH03888.1; -. RBL; BC003888; AAH03888.1; -. RBL; BC003889; AAH03888.1; -. RBL; BR003599; Ig_cl.

R InterPro; IPR003599; Ig_cl.

R InterPro; IPR003596; Ig_MHC.

R InterPro; IPR003596; Ig_wHC.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 1.

R SMART; SM00406; IGC; 1.

R SMART; SM00410; IG_L148; 1.

R SMART; SM00410; IG_L148; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

REMEL; BCO04476; AAR04476.1; -.
R HSSP: PO1857; IB_C1.
R InterPro: IPR003597; Ig_c1.
R InterPro: IPR003500; Ig_like.
R Pfan: PF00047; Id; 3.
R Pfan: PF00047; Id; 3.
R SMART; SM00410; IG_like; 1.
R PROSITE; SM00410; IG_like; 1.
R PROSITE; SM00410; IG_like; 1.
R PROSITE; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.1%; Score 140; DB 4; Length 375; 29.7%; Pred. No. 1.9e-07; Live 24; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                321 DYNSTLRVVSALPIQHQDWASGKEFKCKVNNKALPAPIERTISKPK 366
                                                                                                                                                                         PROSITE; PS00290; TG_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 FSAVGEASICEDDWNSGERFICTVTHTDLPSPLKQTISRPK 244
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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TISSUE-LYMPH, LYMPHOMA;
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Best Local Similarity
Matches 30; Conserv
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Q9BSZ1
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                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.1%; Score 140; DB 4; Length 597; Best Local Similarity 29.7%; Pred. No. 3.3e-07; Matches 30; Conservative 24; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, PO1825; 7FAB.

A InterPro; IPR003599; Ig.

A InterPro; IPR003509; Ig.

A InterPro; IPR003600; Ig_like.

A InterPro; IPR003606; Ig_like.

A InterPro; IPR003606; Ig_like.

A InterPro; IPR003506; Ig_wr.

B Pfam; PF00047; Ig_0.

C SMART; SM00409; IG_1; 4.

C SMART; SM00400; IG_like; 1.

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TISSUE-LYMPH, LYMPHOMA;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002263; AAH02963.1; -.
HSSP; P01825; 7FAB.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LYMPHOMA;
Strauberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006180; AAH06180.1; -.
EMBL; BC001872; AAH01872.1; -.
                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | :: || :: || 426 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK 466
  597 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 AA
PRT;
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=RHABDOMYOSARCOMA;
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NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96GA6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (FROTEIN FOR MGC:20337).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 597;
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003060; Ig_like.
InterPro; IPR003066; Ig_wHC.
InterPro; IPR003596; Ig_w.
InterPro; IPR0047; Ig; 5.
InterPro; IPR00407; Ig; 5.
InterPro; IG; 2.
InterPro; IG; 1.
InterPro; IRR00406; IG; 1.
InterPro; IRR00406; IG; 1.
InterPro; IRR00406; IG; 1.
InterPro; IRR00406; IG_whc; IRR0wn_3.
InterPro; IRR00406; IG_whc; IRR0wn_3.
InterPro; IRR00406; IG_whc; IRR0wn_3.
InterPro; IRR00406; IG_whc; IRR0wn_3.
IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IRR01File IR
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TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.1%; Score 140; DB 4;
29.7%; Pred. No. 3.3e-07;
tive 24; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          597 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.7%
Matches 30; Conservative
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Best Local Similarity 29.7'
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                           9 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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                                                                                                                                                                                                                                     Query Match 24.1%; Score 140; DB 4; Length 613; Best Local Similarity 29.7%; Pred. No. 3.4e-07; Matches 30; Conservative 24; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.1%; Score 140; DB 4; Length 614; 29.7%; Pred. No. 3.4e-07; Live 24; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001) to the EMBL; BC009851; AAH09851.1; -SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -
SEQUENCE 613 AA, 67273 WW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKOTISRPK 461
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TISSUE-PRIMARY B-CELLS FROM TONSILS;
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                           TISSUE-PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNKNOWN (PROTEIN FOR MGC:15420)
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TISSUE=LYMPH, AND LYMPHOMA;
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Best Local Similarity 29.7%
Matches 30; Conservative
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SEQUENCE FROM N.A.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC017356; AAH17356.1; -. Hypothetical protein. SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;
  RE SO SO
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|                                                               | 2;                                                         |                                                                   |
|---------------------------------------------------------------|------------------------------------------------------------|-------------------------------------------------------------------|
|                                                               | ; Gaps                                                     | FNST 68                                                           |
| 24.1%; Score 140; DB 4; Length 618; 29.7%; Pred. No. 3.5e-07; | Matches 30; Conservative 24; Mismatches 45; Indels 2; Gaps | 9 VELEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVOFNWYVDGVEVHNAKTKPREEOFNST 68 |
| Ouery Match<br>Best Local Similarity 29.7%;                   | Matches 30; Conservative                                   | Qy 9 VFLFPPKPKDTLMISRTPEVTC                                       |

QQ Q Q

Search completed: June 21, 2002, 08:59:30 Job time: 1629 sec

in the second

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Gencore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:37:53; Search time 102.05 Seconds

(without alignments)

103.575 Million cell updates/sec

1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138
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Post-processing: Minimum Match 0%
Maximum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database: PIR\_71:\*
1: pIr:\*\*
2: pIr:2:\*
3: pIr:3:\*
4: pIr:4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Minimum DB seq length: 0 Maximum DB seq length: 200000000

|           | Description    | q qamma chain C | , 6    | q qamma-1 | Ig heavy chain V r | . 6  | g gamma-2 chain | g gamma-3 chain | б      | б      | 0      |        | 6      | ס      | g gamma | Ig gamma 1 chain c | 5      | ь      | Ig gamma chain C r | ь    | ъ      | g gamma-3 |       |        | Ig gamma-2b chain | 6      |          |            |       | g      |
|-----------|----------------|-----------------|--------|-----------|--------------------|------|-----------------|-----------------|--------|--------|--------|--------|--------|--------|---------|--------------------|--------|--------|--------------------|------|--------|-----------|-------|--------|-------------------|--------|----------|------------|-------|--------|
| SUMMARIES | ID             | T02             | S31866 | GHHU      | 869339             | G4HU | G2HU            | A60764          | A23511 | G3HUWI | 147160 | 147159 | 147162 | S22080 | 147161  | 147158             | PS0018 | C30554 | GHRB               | G2GP | S31459 | G3MSC     | G3MSM | S06611 | G2MSBM            | G2MS11 | GIMS     | S00847     | GIMSM | PC4436 |
|           | DB             | 7               | 4      | 7         | 7                  | H    | 7               | 7               | 7      | ٦      | ~      | 7      | ~      | 7      | 7       | 7                  | 7      | 7      | П                  | П    | 7      | ٦         | ٦     | 7      |                   |        | <b>~</b> | ~          | -     | 7      |
|           | Length         | 234             | 255    | 330       | 374                | 327  | 326             | 377             | 377    | 289    | 328    | 328    | 277    | 470    | 328     | 328                | 333    | 308    | 323                | 329  | 472    | 329       | 398   | 327    | 405               | 7      | 324      | $^{\circ}$ | 393   | 444    |
|           | Query<br>Match | 4.9             | 4.9    | 4.9       | 4.9                | 4.2  | •               | 1.8             | 1.8    | 4.     | 9.0    | 9.0    | 7.2    | 5.0    | •       | 3.9                | •      | 1.7    | 1.7                | 1.7  | 1.7    | •         | •     | •      | ٠                 | •      | 7.5      | ٠          | ٠     | 7.5    |
| d         | Mai            | ð               | ð      | ð         | 6                  | ð    | 9               | 6               | 9,     | æ      | ~      | ~      | 7      | 7      | 7       | 7                  | 7      | 7      | 7                  | _    | 7      | 7         | _     | ĕ      | ò                 | ò      | ò        | 67         | 67    | 9      |
|           | Score          | ິ               | 557    | 557       | 557                | 55   | •               | 539             | 3      | 519    | 458    | 458    | 453    | 440    | 434     | 434                | 431    | 421    | 421                | 421  | 421    | 418       | 418   | 410    | 397               | 397    | 396      | 366        | 396   | 396    |
|           | Result<br>No.  | -               | 7      | m         | 4                  | S    | 9               | 7               | 80     | 6      | 10     | 11     | 12     | 13     | 14      | 15                 | 16     | 17     | 18                 | 19   | 20     | 21        | 22    | 23     | 24                | 25     | 56       | 27         | 28    | 29     |

Silence of Samma-1 chain C region - synthetic
C.Species : synthetic
A.Note: Homo sapiens (man) gene engineered and expressed in Escherichia coll
C.Species: synthetic
A.Note: Homo sapiens (man) gene engineered and expressed in Escherichia coll
C.Species in Silence of C.Species in Silence in Streeting method for protein-protein interactions of cloned gene produc
A.Reference number: Silence of A.Recession: A.Recession: Silence of A.Reces

94.9%; Score 557; DB 4; Length 255;

Query Match

| Ig gamma-2a chain Ig gamma-1a chain Ig gamma-1a chain Ig gamma-2a chain Ig gamma-2a chain Ig gamma-2b chain Ig gamma-1a chain C Ig gamma-1 chain C Ig gamma-1 chain C Ig gamma-1 chain pre                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ALIGNMENTS  ion - chimpanzee odytes (chimpanzee) steduence_revision 23-Nov-1991 #text_change 16-Jul-1999 stafa, Z.A.; Oestberg, L. 9-322, 1991 sequence of chimpanzee Fc and hinge regions. PT0207; MUID:91287716 IA INC. Oglobulin C region; immunoglobulin homology obulin unoglobulin homology <imm></imm>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | tch 94.9%; Score 557; DB 2; Length 234; al Similarity 94.5%; Pred. No. 3.5e-48; 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0; APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60 |
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| GGMSAB<br>GGMSA<br>GGMSA<br>GGANSA<br>GANGA<br>SO1321<br>SO1321<br>SO1321<br>PSO019<br>PSO019<br>PSO019<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO010<br>PSO01                                                                                                                                                | RESULT 1 PT0207 Ig gamma chain C region - chimpanzee C;Species: Pan troglodytes (chimpanzee) C;Accession: PT0207 R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, Mol. Immunol. 28, 319-322, 1991 A;Title: Nucleotide sequence of chimpanzee A;Reference number: PT0207; MUID:91287716 A;Accession: PT0207 A;Accession: Total CEHRA C;Superfamily: immunoglobulin C region; imm                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Score 557; D Pred. No. 3.5. 2; Mismatches ISRTPEVTCVVVDVS IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII                                                                                                          |
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| 3333<br>3333<br>3356<br>3446<br>3446<br>3456<br>4456<br>4456                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | n - chir<br>ytes (cl<br>gquence, 2.7<br>afa, 2.1<br>322, 199<br>quence (<br>0207; 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| 394<br>391<br>391<br>381<br>381<br>380<br>380<br>276<br>276<br>167 · 5<br>165 · 167                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | SULT 1  207  qamma chain ppecies: Pan ate: 23.Nov. ccession: PT Shrlich, P.H. Chilich Nucleo Reference num Accession: PT Accession: PT Colecule type Residues: 1: Superfamily: Superfamily: Resymords: imm                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | rd O                                                                                                                                                                                                 |
| 0.000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | RESULT 1 PT0207 Ig gamma chain C region - chimpanzee C; Species: Pan troglodytes (chimpanzee) C; Date: 23-Nov-1991 #sequence_revision C; Accession: PT0207 R; Ehrlich, P.H.; Moustafa, Z.A.; Oestbe Mol. Immunol. 28, 319-322, 1991 A; Title: Nuclectide sequence of chimpan A; Reference number: PT0207; MUID:912877 A; Accession: PT0207 A; Molecule type: mRNA A; Residues: 1-234 cERNA A; Residues: 1-234 cERNA C; Superfamily: immunoglobulin C region; C; Keywords: immunoglobulin phomolog                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Query M<br>Best Lo<br>Matches<br>Qy 1<br>Db 25<br>Qy 61<br>Db 85                                                                                                                                     |

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A; Gene: GDB:1GHG1
A; Cross-references: GDB:120085; OMIM:147100
A; Cross-references: GDB:120085; OMIM:147100
A; Cross-references: GDB:120085; OMIM:147100
A; Main diagramer: 14471; 22471
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light ( hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin C region; Immunoglobulin homology
C; Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C; Superfamily: immunoglobulin homology < IM2>
F; 20-6870main: immunoglobulin homology < IM2>
F; 213-210/Domain: immunoglobulin homology < IM2>
F; 243-310/Domain: immunoglobulin homology < IM2>
F; 243-310/Domain: immunoglobulin homology < IM2>
F; 219: 144-204, 250-308/Disulfide bonds: #status experimental
F; 103, Disulfide bonds: interchain (to light chain) #status experimental
F; 103, Disulfide bonds: interchain (to heavy chain) #status experimental
F; 109, 112/Disulfide bonds: interchain (covalent) #status experimental
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A; Wolecule type: protein
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A; Role this sequence has the Gim(3) and Gim(non-1) markers
A; Note: this sequence has the Gim(3) and Gim(non-1) markers
B; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A; Title: The schwarz, J.; Redichel, W.; Hilschmann, N.
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B; Dreker, M.; Schwarz, J.; Redichel, W.; Hilschmann, N.
B; Dreker, M.; Dreker, J.; Dreker
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Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-140, (C', 142-374 <KH2>
A;Coss-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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94.5%; Pred. No. 5.3e-48;
iive 2; Mismatches 4
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                     A; Reference number: A91723; MUID:83289131
A; Coctents: myeloma protein KOL; disulfide bonds
A; Accession: A91723
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Best Local Similarity 94.55
Matches 104; Conservative
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A; Accession: S72664
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A; Molecule type: mRNA
A; Residues: 1-374 < KHA>
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A; Reference number: A90563; MUID:71064024
A; Contents: myeloma protein Eu
A; Accession: B90563
A; Motecule type: protein Eu
A; Residues: 1-96, Rr.)98-135 < CUN>
A; Note: this sequence has the Glm(3) marker, 97-Arg
R; Ritishauser: U; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
B; Rochemistry 9, 3171-3181, 1970
A; Ritile: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque
A; Reference number: A90564; MUID:71064025
A; Contents: Eu
A; Rocession: A90564
A; Molecule type: protein
A; Molecule type: p
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A; Accession: A93433; MULD: 022/4236
A; Redecule type: DNA
A; Realdues: 1-330 eELL>
A; Cross-references: EMBL: 211370
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers,
A; Note: Lys-330 of Has
A; Reference number: S33804
A; References: EMBL: 211370
A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of a A; References number: S33887; MUID: 83001943
A; Residues: 88-113; 235-330 cTAK>
A; Residues: 88-113; 235-330 cTAK>
A; Residues: 88-113; 235-330 cTAK>
A; Residues: B8-113; 235-
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A; Molecule type: protein
A; Residues: 1.34, '0', 36-96, 'K', 98-115, '0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Note: this sequence has the Glm(17) and Glm(1) markers
A; Note: this sequence has the Glm(17, 111schmann, N.
B; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
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C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
                                                                                           Gaps
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                     Pred. No. 3.9e-48;
2; Mismatches 4;
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A;Contents: myeloma protein Nie
A;Accession: B91668
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                            94.58;
                                                                                                  104; Conservative
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A;Gene: GDB:IGHG2
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A; Cross-references: GDB:I19340; OMIM:147130
A; Cross-references: GDB:I19340; OMIM:147130
A; Map position: 14432.33-14432.33
A; Introns: 99/1; Introns: 197; Introns: Intr
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A; Residues: 1-327 <ELL>
A; Note: the sequence was determined from the germline gene
A; Note: the sequence was determined from the germline gene
B; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: mimunoglobulin sublclasses. Partial amino acid sequence of the constant.
A; Reference number: A90249; MUID:70207560
A; Accession: A90249
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C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
C;Accession, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
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F:240-307/Domain: immunoglobulin homology <IM3>
F:240-3107/Domain: immunoglobulin homology <IM3>
F:240-3107/Domain: immunoglobulin homology <IM3>
F:140-1307/Lander interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
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A;Reference number: A90933; MUID:83157104
A;Accession: A90933
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Score 557; DB 2;
Pred. No. 6.1e-48;
2; Mismatches 4
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    Query Match
Best Local Similarity 94.5%;
Matches 104; Conservative
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A; Residues: 1-30;81-326 <PIN>
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Best Local Similarity
Matches 104; Conserv
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A; Molecule type: protein
A; Residues: 1-24, Ev. 26-57, EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 1
A; Residues: 1-24, Ev. 26-57, 'EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 1
A; Note: this sequence heas since been revised
R; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli
A; Reference number: A93132; MUID:80114419
A; Contents: Zie
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A, Realdues: 238-275 (4007-
A), Realdues: 238-275 (4007-
R: Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A, Reference number: A94591
A, Reference number: A94591
A, Note: the revised sequence differs from that shown in having 60-Ala and in the amid
                                                                                                                                                                                                                                                                                                         A Molecule type: DNA A Read A Molecule type: DNA A Molecule type: DNA A Molecule type: DNA A Residues: 1-326 cell. A Molecule type: GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; PID:96066056 A; Note: Lys-326 is probably removed posttranslationally B; Nang, A.C.; Tung, E.; Fudenberg, H.H. J. Immunol. 125, 1048-1054, 1980 A; Title: The primary structure of a human 19G2 heavy chain: genetic, evolutionary, an A; Reference number: A2809; MUID:81007873 A; Contents: myeloma protein Til
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A;Map position: 14q32.33-14q32.33
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin c region; immunoglobulin c region; heterotetramer; immunoglobulin F;20-05/Domain: immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Reference number: A93906; MUID:82197621
A;Accession: A93906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Wolecule type: protein
A; Residues: 1-19, 0', 21-57, 2', 59, 'A', 61-193,'D', 195-325 <WAN>
A; Note: Trp-156 is at or near the complement-binding site
B; Connell, G.E.; Parr, D.M.; Hoffmann, T.
Can. J. Blochem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of Reference number: A90752; MUID:80001357
A; Reference number: A90752; MUID:80001357
A; Contents: myeloma protein Zie
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F:27-83.440-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Biochem. J. 121, 217-225, 1971
ArTitle: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A.Reference number: A90253; WIDD:72033500
A.Reference number: A90253; WIDD:72033500
A.Contents: annotation; myeloma protein Sa, disulfide bonds
R.Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A.Fille: Structural studies of immunoglobulin G.
A.Reference number: A93137; MUID:69064124
A.Reference number: Sa, disulfide bonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;133-202/Domain: immunoglobulin homology <IM2>F;239-306/Domain: immunoglobulin homology <IM3>
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Alwote: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in Bloches. Bloches
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A; Residues: 1-289 <FRA>
A; Nete: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A; Note: this protein lacks most of the V region and all of the CHI region. Residue 12
A; Note: the sequence of residues 42-76 was taken from the reference that follows
B; Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A; Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat
A; Reference number: A02219; MUID: 77118561
A; Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Accession: A2219
A)Molecule type: protein
A)Residues: 12-97 AMC>
A)Note: the hinge region in gamma-3 chains is about four times as long as in other idue segment (12-28)
                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3
                                                                                                                                                                                                                                         Gramma-3 heavy chain disease proteins - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999 C;Accession: A90442; A92219; A90198; A93915; A02149 R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C. Biochemistry 19, 4304-4308, 1980
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                                                             Length 289;
                           PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 519; DB 1; L
Pred. No. 2.8e-44;
9; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A90442; MUID:81021548
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
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86.4%;
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95; Conserv
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Best Local
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Ig gamma-3 chain C region (allotype G3m(b)) - human
G'Species: Homo sapiens (man)
C'Species: 18-Dec-1987 #sequence_revision 20-Dec-1987 #text_change 23-Jul-1999
C'Accession: A23511
R'Huck, S.; Fort, P.; Crawfoord, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A'Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
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                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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                                                                                                                           61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                             PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 377
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Pred. No. 3.9e-46;
4; Mismatches 6; Indels
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R; Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A; Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, A; Reference number: A60764; MUID:90007613
A; Accession: A60764
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule type: DNA
A.Residues: 1-377 <HUC>
S.Weperfamily: immunoglobulin C region; immunc
C.Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                 form LAT - human
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90.9%;
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Matches 100; Conserv
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A; Residues: 1-377 <HUC>
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Best Local Sim
Matches 100;
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A; Residues: 1-470 <SANA
A; Residues: 1-470 <SANA
A; Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
A; Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R; Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
Mol. Immunol. 26, 841-850, 1989
A; Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1
A; Reference number: S06610; MUID:90097956
A; Accession: S06610
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N'Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
                                                         C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147162
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence number: 147158; MUID:95015845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Reywords: glycoprotéin; heterotetramer; immunoglobulin; membrane protein F;161-225/Domain: immunoglobulin homology <IMM> F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: U03782; NID: 9433129; PIDN: AAA52220.1; PID: 9433130
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A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membr
F;161-225/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline
C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.2%; Score 453; DB 2; 77.9%; Pred. No. 1e-37; iive 14; Mismatches
                                       gamma 4 chain constant region - pig (fragment)
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72.58;
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A; Accession: $22080
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nes 79; Conserv
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C; Superfamily
F; 82-151/Doma
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C:Species: Sus scrofa domestica (domestic pig)
C:Species: Sus scrofa domestic pig)
C:Sacession: I47160
R:Kacskovics, I:Sun, J:Butler, J.E.
J: Immunol: 153, 355-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a SA;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a SA;Tetus: Preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Gessidues: 1-328 <AAC>
A;Gessidues: 1-328 <AAC>
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Gene: IgGSb
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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Matches 82; Conservative
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Search completed: June 21, 2002, 08:37:53 Job time: 427 sec
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J. Immunol. 153, 3565-3573, 1994
A. Timunol. 153, 3565-3573, 1994
A. Reference number: 147158; MUID:95015845
A. Accession: 147158
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
A. Residues: 1-328 < KAC>
A. Residues: 1-328 < KAC>
A. Cross-treferences: EMBL:U03778; NID:9433121; PIDN:AAA52216.1; PID:9433122
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18 Samma 1 chain constant region - pig (fragment)
C.Speciles: Sus scrofa domestica (domestic pig)
C.Speciles: Sus scrofa domestica (domestic pig)
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C.Accession: 147158
C.Accession: I47158
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                Length 328;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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MEDLYNE-71064027; PubMed-4923144;
Gall W.E., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. X. "The covalent structure of a human gamma G-immunoglobulin. X.
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GenCore version
Copyright (c) 1993 - 2000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                               "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";

Blochemistry 20:2361-2370(1981).

"HISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, 6 THE GIM(1) MARKERS, 239-D 6 241-L. KOL 6 EU SEQUENCES HAVE THE GIM(3) MARKER F THE GIM (NON-1) MARKERS.

"HISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 6 272.

"HISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
                                                Dreker L., Schwarz J., Reichel W., Hilschmann N.; Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein. The L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                  MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; 3D-structure. 1 1 1 1 DOMAIN 1 98 CH1.
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INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
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L -> M (IN GIM(NON-1) MARKER).
/FIIGHVAR_003888.
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REMOVED POST-TRANSLATIONALLY.
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/FIId=VAR.003886.
D -> F / T
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                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; Pubmed-7236608;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00228; AAC82527.1; ALT_INIT.
PIR; A02146; GHHU.
PDB; IFC1; 15-JUL-92.
PDB; IFC2; 15-JUL-92.
MIM; 147100; -.
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HINGE.
CH2.
CH3.
                             DISULFIDE BONDS.
MEDLINE=77070267; PubMed=1002129;
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2
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Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the
Constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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MEDLINE-83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 DNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                                                                                 36106 MW; 3770EE106C2FA33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 557; DB 1;
Pred. No. 6.4e-49;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Best Local Similarity 94.5%;
Matches 104; Conservative
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Best Local Similarity
NCBI_TaxID=9606;
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P01861;
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Cell 29:671-679(1982).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ellison J.W., Hood L.E.; "Linkage and sequence homology of two human immunoglobulin gamma "Linkage and sequence homology of two human constant region genes."; Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Fetal liver;
MEDLINE-83001943; PubMed-6811139;
Takahashi N., Udda S., Obata M., Nikaido T., Nakai S., Honjo T.;
"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 327;
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35940 MW; 3EDBD811EF208E7A CRC64;
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                                                                                                                                                                 PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region.
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-2 chain C region.
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CH2.
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                                                                                                      Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_C1.
Interpro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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Best Local Similarity 94.5
Matches 104; Conservative
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327 AA;
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MIM; 147130;
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P01859;
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                              TISSUE-Fetal liver;
MEDLINE-84235992; PubMed-6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";
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MEDITNE-72033500; PubMed-4940472;
Milstein C., Frangione B.;
"Disulphide bridges of the heavy chain of human immunoglobulin G2.";
Biochem. J. 121:217-225(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G., "Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
MEDLINE-80001357; PubMed-113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human igG2 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 238-275 (2IE).
MEDLINE-801141419; PubMed-118920;
Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human
                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
MEDLINE-81007873; PubMed-6774012;
Wang A.-C., Tung E., Fudenberg H.H.;
"The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 25; 59; 60 AND 264-268 (ZIE). Hofmann T., Parr D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
SEQUENCE OF 99-177 AND 310-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem. 228:886-893(1995)
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MEDLINE-95255298; PubMed-7737190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Immunol. 16:923-925(1979)
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
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REMOVED POST-TRANSLATIONALLY (PROBABLE).
S -> A (IN MYELOMA PROTEINS TIL & ZIE).
TIT-VAR_003889.
C -> S (IN REF. 3).
8310878C6878CF9C CRC64;
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                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
Prinary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
Primary structure of the 'hinge' region of human 1963. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                          1;
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CHAIN).
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HINGE.
CH2.
CH3.
INTERCHAIN (WITH A LIGHT CHAIN).
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region (Heavy chain disease protein) (HDC)
1GGHG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-77021516; PubMed-823945; Verbil F., Franklin E.C., Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C., "The amino acid sequence of 'heavy chain disease' protein 20C. Structure of the Fc fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                               CHAIN)
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Pred. No. 1.5e-47;
5; Mismatches 2.
              Immunoglobulin C region
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MEDLINE-81021548; Pubmed-6774747;
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 PS00290; IG_MHC;
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Matches 102; Conservative
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                                                                                                                                                                                                                                                                 -:- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
AND ALL OF THE CHI REGION.
-!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
GAMMA-3 HEAVY CHAINS.
-!- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
OR ANOTHER GAMMA CHAIN SUBCLASS.
-!- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                                                          Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain; Immunoglobulin C region; Glycoprotein; Repeat.
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INTERCHAIN (WITH HEAVY CHAIN DIMER).
                  Franklin E.C., Hood L., Buxbaum J.N.; "Gamma Heavy chain disease in man: cDNA sequence supports partial gene deletion model.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .).
REMOVED POST-TRANSLATIONALLY
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Alexander A., Steinmetz M., Barritault D., Frangione B.,
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FTIG-VAR 003890.

P -> L (IN OMM).

FTIG-VAR 003891.

F -> Y (IN OMM).

FTIG-VAR 003892.

T -> A (IN OMM).
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CH2.
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SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immunoglobulin domain; Immun
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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HSSP; P01857; 1FC1.
MIM; 147120; -.
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AT BROOM M
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Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                  Length 290;
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                                                                         F -> Y (IN OMM).
/FTId=VAR_003896.
E69CBC95705B2F46 CRC64;
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69.7%; Pred. No. 3.2e-36;
iive 19; Mismatches 14;
                                                                                                                                                                                Score 519; DB 1;
Pred. No. 3.7e-45;
                                   MISSING (IN ZUC)
/FTId=VAR_003895.
F -> Y (IN OMM).
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UGL-1999 (Rel. 38, Last annotation update)
19 gamma-2B chain C region.
Rattus norvegicus (Rat).
N (IN OMM)
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MEDLINE-89232738; PubMed-3149946;
                                                                                                                       MM.
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Mammalia; Eutheria; Rodentia;
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86.4%;
                                                                                                                     32331
                                                                                                                                                                            Query Match
Best Local Similarity 86.44
Matches 95; Conservative
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147
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333 AA;
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Best Local Similarity
Matches 76; Conserv
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227
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P20761;
                                       VARIANT
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                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-128.
MEDLINE=76135469; PubMed=1243651;
MEDLINE=76135469; PubMed=1243651;
Pratt D.M., Mole L.E.;
"Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILE-8403030; PubMed-6313520;
BETISLE-84 Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit 19G heavy chain from the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stockholm (1967).
-!- MISCELLANBOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
104-THR, AND. THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
MARKERS AND REF.5 THE E15 MARKER.
                                                                                                            Ig gamma chain C region.
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit
imminoraloulin G.".
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 88-266 FROM N.A.
MEDLINE=83299917; PubMed=6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 196: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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MARKER).
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InterPro: IPR003006; Ig_MHC.
InterPro: IPR003006; Ig_C1.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGC1; 2.
PROSITE; PS00200; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
                                                            (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
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E15 M
REF.
                               323 AA
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SEQUENCE OF 129-131 AND 155-322.
                                                                                                                                                                                                                                                                                    ſmmunogenetics 18:387-397(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. J. 116:249-259(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M16426; AAA31289.1; -.
                                STANDARD;
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185
48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin G.
                                                                                                                                                                         NCBI_TaxID=9986;
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185
48
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                                                            21-JUL-1986
21-JUL-1986
                                                                                            15-JUL-1999
                               GC_RABIT
P01870;
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RESULT
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                                                                     Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin."; Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED GUINEA PIGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=85027161; Pubmed=6092053;
MEDLINE=85027161; Rimm D., Der-Balan G.P., Martinez H.M.,
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine 1gG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                 INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                domain; Immunoglobulin C region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.7%; Score 421; DB 1; Length 32 Best Local Similarity 71.6%; Pred. No. 3.2e-35; Matches 78; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 36074 MW; 5D231B7164D1FBA9 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region, secreted form.
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                                           DISULFIDE BONDS.
MEDLINE=71058474; PubMed=4922544;
                Biochemistry 13:4804-4811(1974)
                                                                                                                                     PIR; A02151; GZGP.
HSSP; P01772; 2FB4.
InterPro; IPR00306597; Ig_Cl.
InterPro; IPR003507; Ig_Cl.
InterPro; IPR003600; Ig_Llke.
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Mammalia; Eutheria; Rodentia;
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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329 AA;
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DISULFID 105
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P22436;
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                                                                                                                                                                                                                                                                                     "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal and hinge region cyanogen bromide fragments.";
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birshtein B.K., Hussain Q.Z., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cystine joining heavy and light chains.";
                                                                                                                                                                                                                                                                       2 PPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-7503672; Pubmed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 227-311.
MEDLINE-75036073; PubMed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                               GC2_CAVPO STANDARD; PRT; 329 AA.
GC2_CAVPO GC2_CAVPO
PO1862;
PO1862;
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1989 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Gavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Hystricognathi; Cavidae; Cavia.
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(IN REF. 2).
IN REF. 3 AND 4).
IN REF. 5).
IN REF. 3 AND 5).
                                                                                                                                                              -> S (IN REF. 5).
69E8AA118D579A8B CRC64;
                                      E (IN REF. 5).

D (IN REF. 5).

O (IN REF. 5).

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O (IN REF. 5).

D (IN REF. 5).

V (IN REF. 5).

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V (IN REF. 5).
                                                                                                                                                                                                                                             14; Mismatches
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Turner K.J., Cebra J.J.;
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                                                                                                                                                                            35404 MW;
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les 76; Conservative
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                                                                                                                                                                            323 AA;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
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Best Local Similarity
Matches 76; Conserv
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DOMAIN
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GCB_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine 19G3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                      Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-84041483; Pubmed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    F45827174182BAD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.2%; Score 418; DB 1; 68.5%; Pred. No. 6.4e-35; iive 15; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-0CT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
19 gamma - 3 chain C region, membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 AA
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Nucleic Acids Res. 11:6775-6785(1983).
                                                                                                                                                                                                                                                                                                                               CH1.
HINGE.
CH2.
       -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J00451; AAB59655.1; -. BMBL; V01286; CAA24767.1; ALT_SEQ. PIR; A02155; GANSM. HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                CH3
                                                   HSSP, P01857; 1FC1.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART: SM00410; IG_like; 1.
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223
327
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Best Local Similarity
Matches 76; Conserv
EMBL; .J00451; -; NV
PIR; B02156; G3MSC
HSSP; P01857; 1FCL
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SEQUENCE FROM N.A. (B ALLELE).
MEDLINE-82173203; PubMed-6803173;
Ollo R., Rougeon F.;
"Mouse immunoglobulin allotypes: post-duplication divergence of gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 PPGNILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWT 171
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SEQUENCE FROM N.A. (MPC 11).
SEQUENCE FROM N.A. (MPC 11).
Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
"Structure of the constant and 3' untranslated regions of the murine gamma 2b heavy chain messenger RNA.";
Science 206:1299-1303(1979).
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MEDLINE-80081502; PubMed-117549;
Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
Tsequence of the cloned gene for the constant region of murine gamma
2b immunoglobulin heavy chain.";
Science 206:1303-1306(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-80120716; PubMed-6766534; Yakahashi N., Obata M., Honjo T.; Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.; "Complete nucleofide sequence of immunoglobulin gamma2b chain gene cloned from newborn nouse DNA."; Nature 283:786-789(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
1-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
1g gamma-2B chain C region.
1g gamma-2B chain C region.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGCl; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
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Pred. No. 7.9e-35;
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HINGE.
CH2.
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68.5%;
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RARE TEREFEER AND BRANK 
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REMOVED POST-TRANSLATIONALLY (PROBABLE).
Q -> R (IN B ALLELE).
T -> A (IN B ALLELE).
M -> D (IN B ALLELE).
M -> I (IN B ALLELE).
L -> S (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
My; 7D879662607C356E CRC64;
                                                                                             MEDLINE-94216359; PubMed=7512967;

Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,

Irimura T., Takahashi N., Kato K., Arata Y.;

"O-glycosylation in hinge region of mouse immunoglobulin G2b.";

J. Biol. Chem. 269:12345-12350(1994).

-! PPM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS

MODIFIED WITH 2 SIALIC ACID RESIDUES.
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                                                                                                                                                                                                                                                                      -!- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
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Sciurognathi; Muridae; Murinae; Mus.
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INTERPO: IPRO03006; Ig_MHC.
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2B chain C region, membrane-bound form.
Aus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra'
Mammalia; Eutheria; Rodentia; Sciurognathi; Muric
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  2a and gamma 2b chain genes.";
Nature 296:761-763(1982).
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336 AA;
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                                                                                                                                                                                                                                                            CELL 26:19-27(1981).
-1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES SPORTED SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDARY SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS. A LESS ABUNDARY SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF THE MEMBRANE GAMMA
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"Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                     SEQUENCE OF 335-378 FROM N.A. MEDINE-82115295; PubMed-6799207; Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.,
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CYTOPLASMIC (POTENTIAL).
89B3CF0A9B6D49FA CRC64;
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HSSP, PQ1857; IPC1.
MGD; MGI:96445; IPC1.
MGD; MGI:96445; IPC1.
InterPro; IPR003509; Ig_MHC.
InterPro; IPR003509; Ig_Like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_Like; 1.
SWART; SM00407; IG_MHC; 1.
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RESULT 12

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P20762;
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MEDINE-80012837, PubMed-113776;
ROGERS J., Clarke P., Salser M.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDILINE-8020559; PubMed-670552;
Obbta M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                 "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene."; Cell 18:559-568(1979).
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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R EMBL, V00793; CAA24173.1; -.
R EMBL, V00793; CAA24173.1; -.
R EMBL, V00793; CAA24175.1; -.
R EMBL, V00793; CAA24175.1; -.
R EMBL, V00795; CAA24175.1; -.
R EMBL, V00795; CAA24176.1; -.
R EMBL, V00795; CAA24176.1; -.
R HSSP, P01842; F78B.
R GLycosuitebB; P01868; -.
R MGD; MGI:96446; Igh-4.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003006; Ig_MC.
R InterPro; IPR003006; Ig_MC.
R PFABL; PS00290; IG_MHC.
R PROSITE; PS00290; IG_MHC: 1.
M Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
M Alternative Splicing.
                                                                                                                                                                                                                                                                                     MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adetugbo K.; "Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma gammal chain."; J. Biol. Chem. 253:6068-6075(1978).
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"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850(1972).
                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mus musculus (Mouse).
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MEDLINE-73008889; PubMed-5073237;
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                         STANDARD;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-88166903; PubMed-3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
                                                                                                INTERCHAIN (WITH A LIGHT CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
11 gamma-2C chain C region.
Rattus norvegicus (Rat).
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    CH1.
HINGE.
CH2.
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35704 MW;
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P01864;
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MEDLINE—8222190; Pubmed=6283537;
Wanawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-!-ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPRAST OF NCODE MEMBRANE-BOUND LIN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
                                                                                                                                                 0; Gaps
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MEDLINE-80045036; PubMed=115593;
MEDLINE-80045036; PubMed=115593;
MOIO T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Amoro Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 323-393 FROM N.A. MEDLINE-82197626; PubMed-6804950; Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.; "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 323-366 FROM N.A.
MEDLINE-82115295; PubMed-6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Elsenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
                                                   (WITH A HEAVY CHAIN).
                               INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                         67.5%; Score 396; DB 1; Length 329; 67.6%; Pred. No. 1e-32;
                                                                                                                                              17; Indels
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                                                                                           36571 MW; 5FCD7B7933850773 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY - Chain C region, membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                    Pred No. 1e-32;
17; Mismatches
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                                                  INTERCHAIN
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329 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Bioropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                          HSSP, P01842; 7FAB.
MGD; MGI:96446; Igh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
Pfan; PF00047; Ig.2.
SMART; SM00407; IGc1; 2.
SMART; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing; Transmembrane.
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HEAVY CHAIN).
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4CC88343B7A1CE27 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, B allele.
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Search completed: June 21, 2002, 09:00:23 Job time: 1447 sec

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61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

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L; Length 335;
32;
21; Indels

Ouery Match 67.1%; Score 394; DB 1; Best Local Similarity 64.5%; Pred. No. 1.7e-32; Matches 71; Conservative 18; Mismatches 21 THIS PAGE BLANK (USPTO)

Run

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096kx8 homo sapien
096dk0 homo sapien
099m1 mus musculu
09brv0 homo sapien
091207 mus musculu
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099kx4 mus musculu
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09v787 drosophila
09r1a5 mus muscu
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"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
EMBL: AF272774; AAK58686.1; ...
SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
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Pred. No. 3.3e-53;
2; Mismatches 4;
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Q96DK0
Q99M11
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Q99LA6
Q91WP5
Q91WT1
Q91X92
Q91X82
Q91WR1
Q9DCD9
Q91XE1
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Q91WS9
Q91WF8
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Q99KA4
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94.5%;
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
NCBI_TaxID=9606;
  121.5
1121.5
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                               437 AA;
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                                                                                                                                                                                                                                      "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c.mu, c.gamma, c.epsilon and c.alpha genes."; Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGGPSVFLFPPKPRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           091205 PRELIMINARY; PRT; 473 AA.
091205
01-205.2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Mus musculus (Mouse).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                            Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OCBI_TaxID=9796;
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MEDLINE-98383416; Pubmed-9717671;
Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 473;
                                                                                                                                                                                                                                                                                                                                         Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Indels
                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                    Wagner B.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO10327: AAH10327.1; -
Hypothetical protein.
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                               SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
                                                                                                                                                                                                                                                                                                                                    78.0%; Score 458; DB 6; 73.6%; Pred. No. 1.3e-42; tive 16; Mismatches 13;
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67.6%; Score 397; DB 11;
Best Local Similarity 65.5%; Pred. No. 1.1e-35;
Matches 72; Conservative 17; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                            81; Conservative
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                                                                                 Equus caballus (Horse).
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Matches 81; Conservat
                                                                                                                                          SEQUENCE FROM N.A.
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                                                        FRAGMENT).
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                                                                                                                                                                                                                                            Wilde K.G., Yu X., Exramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclo antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scrv).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF15272; AAD40243.1;
ENSP; PO1842, 7FAB
InterPro; IPR003606; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.5%; Score 396; DB 11; Length 437; llarity 67.6%; Pred. No. 1.3e-35; Conservative 19; Mismatches 14; Indels
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48142 MW; 5C3A7BB3EE7D697C CRC64;
                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMA1 HERVY CHAIN OF MAB7 (FRAGMENT)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
437 AA.
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SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
  PRT;
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InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 3.
SMART; SM00409; IG; 2.
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Query Match
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Matches
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                                                                                                                                  Matches
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Q99L31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                            67.5%; Score 396; DB 11; Length 463; 67.6%; Pred. No. 1.4e-35; ive 19; Mismatches 14; Indels
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SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MUN UNKNOWN_1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
SWART; SW00407; IGC1; 2.
SWART; SW00406; IGV; 1.
SWART; SW00410; IG_LIKe; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003006; Ig_MC.
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EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
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Best Local Similarity 67.69
Matches 69; Conservative
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Q9D8L4
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                                                                                                            Gaps
                                                                                      1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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          Length 473;
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                                                                                                                                                                                        Indels
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF0001; ig; 4. -3-...
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_11ke; 1.
PROSITE: PROD200; IG_MHC; UNKNOWN_1, SEQUENCE 468 AA, 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
  Score 394; DB 11;
Pred. No. 2.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.1%; Score 382; DB 11;
63.6%; Pred. No. 5.2e-34;
11ve 18; Mismatches 22;
67.1%; Score ....
64.5%; Pred. No. 2.4e-
.tive 18; Mismatches
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_HHC.
InterPro; IPR003596; Ig_HC.
                                                 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70; Conservative
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Q9BQB8;
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Q9BU10
                    RESULT
                              29BQB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human),
busharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                    0;
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;
                                                                                                                                                                                                                                          Length 473;
                                                                                                                                                                                                                                                                                                                                                             317 THREDYNSTLRVVSALPIQHQDWASGKEFKCKVNNKALPAPIERTISKPK 366
                                                                                                                                                                                                                                                                                                                                              61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.5%; Score 138; DB 4; Length 375; 28.7%; Pred. No. 4.5e-07; Live 25; Mismatches 45; Indels
                                                                                                                                                                                                                                                                    22; Indels
                the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO04475, AAH04476.1;
HSSP; PO1857; 1FC1.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003500; Ig_like.
InterPro; IPR003066; Ig_MHC.
                                                                                                                 Pfam; PF00047; 19; 4. -2-
SMART; SM00409; IG; 2.
SMART; SM00407; IGcl; 3.
SMART; SM00406; IGv.1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 protein.
375 AA; 41314 MW; BIAOA0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BS21;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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;; Pred. No. 5.2e-34;
18; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                          375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfan: PF00047; 1g; 3.
SMAR: SM00407; 1g; 3.
SMAR: SM00400; IGc1; 3.
SMAR: SM00410; IGc1; 3.
PROSITE: PS00290: IG_MHC; UNKNOWN_3.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL 41.3 KDA PROTEIN.
                                                InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MGC.
InterPro; IPR003596; Ig_WG.
                                                                                                                                                                                                                                         65.18;
63.68;
Strausberg R.;
Submitted (FEB-2001) to the
EMBL; BC003888; AAH03888.1;
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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TISSUE-LYMPH, LYMPHOMA;
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hes 29; Conserv
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Best Local Si
Matches 29;
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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
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01-JUN-2001 (TYEMBLrel. 17, Created)
01-JUN-2001 (TYEMBLrel. 17, Last sequence update)
01-DEC-2001 (TYEMBLREL. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
HOMO Saplens (Human).
BUKARYOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | InterPro; IPR003599; Ig. |
| InterPro; IPR003599; Ig. |
| InterPro; IPR003599; Ig. |
| InterPro; IPR003506; Ig_like. |
| InterPro; IPR003066; Ig_like. |
| InterPro; IPR003066; Ig_v. |
| InterPro; IPR0047; Ig; 5. |
| SMART; SM00407; IGcl, 4. |
| SMART; SM00406; IGv, 1. |
| SMART; SM00410; IG_like; I. |
| SPROSITE; PS00290; IG_like; I. |
| SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.5%; Score 138; DB 4; Length 59 Best Local Similarity 28.7%; Pred. No. 8.1e-07; Matches 29; Conservative 25; Mismatches 45; Indels
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-RHABDOMYOSARCOMA;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC0061872; AAH06180.1; EMBL; BC0061872; AAH01872.1; -.
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1; -.
HSSP; P01825; JFAB.
InterPro; IPR003599; Ig.
                                                                    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
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                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=LYMPH, LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRONGEAVKTHTNISESHPNAT 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
HYPOTHETICAL 65.0 KDA PROTEIN.
EUNA SPECIAL (Human).
EUNA SPECIAL (Human).
ENA SPECIAL (Treation of the special of the sp
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:20337).
HOMO Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.5%; Score 138; DB 4; Length 59
28.7%; Pred. No. 8.1e-07;
tive 25; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                           ll protein.
597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
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                                                                                                                      Pfam; PF00047; 1g; 5.
SMART; SM00409; 1G; 2.
SMART; SM00407; 1Gc1; 4.
SMART; SM00406; 1Gc1; 4.
SMART; SM00410; 1G_11ke; 1.
PROSITE; PS00290; 1G_MHC; UNKNOWN_3.
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TISSUE-PRIMARY B-CELLS FROM TONSILS;
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Ig_c1.
Ig_like.
                                                              InterPro; IPR003006; Ig_MHC.
                                                                                                    IPR003596; Ig_v.
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Best Local Similarity 28.7³
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                           Hypothetical
SEQUENCE 59
                                                                                                    InterPro;
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Q96EY0
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Q96BB9
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Gaps
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HYPOTHETICAL 67.8 KDA PROTEIN.
HYPOTHETICAL 67.8 KDA PROTEIN.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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                                                                                                                                                                                                                          23.5%; Score 138; DB 4; Length 613; 28.7%; Pred. No. 8.3e-07; ive 25; Mismatches 45; Indels
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                      Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC01857; AAH11857.1; -.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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TISSUE=PRIMARY B-CELLS FROM TONSILS;
                              TISSUE=PRIMARY B-CELLS FROM TONSILS;
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TISSUE-LYMPH, AND LYMPHOMA;
Strausberg R.;
                                                                                                                                                                                                                             Query Match 23.5% Best Local Similarity 28.7% Matches 29; Conservative
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Best Local Similarity 28.7%
Matches 29; Conservative
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SEQUENCE FROM N.A.
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Search completed: June 21, 2002, 08:59:30 Job time: 1629 sec

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AAY54998 standard; protein; 110 AA.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                    US-09-674-857-3
587
                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

|        |       | ф     |        |    |          |                  |
|--------|-------|-------|--------|----|----------|------------------|
| Result | ,     | Query | Query  |    |          |                  |
| NO.    | Score | Match | Length | BB | QI       | Description      |
|        | 576   |       | 110    | 21 | AAY54998 | Mutated CH2 sequ |
| 7      | 570.5 |       | 109    | 21 |          | Mutated CH2 sequ |
| m      | 562   |       | 468    | 20 |          | D9D10 heavy chai |
| 4      | 562   |       | 488    | 21 |          | Human FGF-RI Ext |
| Ŋ      | 562   |       | 497    | 21 |          | Human FGF-RI Ext |
| 9      | 562   |       | 525    | 21 |          | Human FGF-RI Ext |
| 7      | 562   | 95.7  | 711    | 20 | AAW85692 | MoTAbII fusion p |
| 80     | 558   |       | 251    | 20 |          | Modified human I |
| 6      | 558   |       | 251    | 20 |          | Modified human I |
| 10     | 558   |       | 251    | 21 |          | Amino acid seque |
| 11     | 558   |       | 559    | 22 |          | IL-20RA-I9 gamma |

uen uen in in tra tra tra tra gro IgG enc

| Human IL-20RA/immu<br>Human IL-20RA-I9 9 | Human immunoglobul | Undefined ORF2 enc | Human IgG1 Fcgamma | Immunoglobulin G1 | Human immunoglobul | Human IgG1 Fc regi | _        | IgG1 Fc protein us | Human IgG1 Fc prot | FC       |          | Human immunoglobul | Fc region of human | Fc region of human | Human immunoglobul | Native IgG Fc regi | FC       | Human IgG Fc 1 all | IgG Fc 1 a |          | IgG1     | Sequence of human | ppnJ     | F.C      | Human IgG1 Fc chai | Human IgG1 Fc regi | Human IgG1 hinge/F |          | Human immunoglobul | Human immunoglobul | gr       | Human partial 19G1 |
|------------------------------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|------------|----------|----------|-------------------|----------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|--------------------|
| AAU04062<br>AAB85274                     | AAR27680           | AAR41684           | AAY42621           | AAR87023          | AAR97264           | AAW02305           | AAW47354 | AAY23637           | AAW92411           | AAY99937 | AAY97182 | AAY97250           | AAB03809           | AAB62062           | AAY72750           | AAB07474           | AAB07475 | AAB67201           | AAB67202   | AAB76421 | AAB76422 | AAP70173          | AAP82508 | AAB16955 | AAY96529           | AAB98953           | AAW26232           | AAB28690 | AAY95579           | AAY70251           | AAE02642 | AAY72915           |
| 22                                       | 13                 | 14                 | 20                 | 16                | 17                 | 17                 | 19       | 20                 | 20                 | 21       | 21       | 21                 | 21                 | 22                 | 22                 | 21                 | 21       | 22                 | 22         | 22       |          |                   |          |          | 21                 | 22                 | 18                 | 21       | 21                 | 21                 | 22       | 22                 |
| 594<br>594                               | 110                | 110                | 116                | 212               | 212                | 212                | 212      | 212                | 212                | 212      | 212      | 212                | 212                | 212                | 212                | 218                | 218      | 218                | 218        | 218      | 218      | 224               | 224      | 228      | 228                | 228                | 232                | 232      | 232                | 232                | 232      | 232                |
| 95.1<br>95.1                             | 4                  | 4.                 | 4                  | 4                 | 4                  | 4                  | 4.       | 4                  | 4                  | 4        | 4.       | 4                  | 4                  | 4.                 | 4                  | 4                  | 4        | 4.                 | 4.         | 4.       | 4        | 4                 | 4        | 4        | 4                  | 4.                 | 4.                 | 4.       | 4                  | 4                  | 4        | 4                  |
| 558<br>558                               | 557                | 557                | 557                | 557               | 557                | 557                | 557      | 557                | 557                | 557      | 557      | 557                | 557                | 557                | 557                | 557                | 557      | 557                | 557        | ß        | 557      | 557               | 557      | 557      | 557                | 557                | 557                | 557      | 557                | 557                | 557      | 557                |
| 12                                       | 14                 | 15                 | 16                 | 17                | 18                 | 19                 | 20       | 21                 | 22                 | 23       | 24       | 25                 | 26                 | 27                 | 28                 | 29                 | 30       | 31                 | 32         | 33       | 34       | 35                | 36       | 37       | 38                 | 39                 | 40                 | 41       | 42                 | 43                 | 44       | 45                 |

## ALIGNMENTS

cell mediated destruction; human; immunoglobulin G; IgG heavy chain; cell mediated destruction; human; immunoglobulin G; IgG heavy chain; crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; attoimmune disease; asthma; allergy; alloimmune disorder; autoimmune hamolytic anaemia; inflammatory disease; neconatral alloimmune thrombocytopeania; arthritis; erythroblastosis foetalis; sickle cell anaemia; coronary artery occlusion. Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD. Clark MR, Williamson LM; Mutated CH2 sequence Gldeltaac. 99WO-GB01441. 98GB-0009951 07-MAY-1999; 08-MAY-1998; W09958572-A1 18-NOV-1999. Armour KL, Synthetic.  99WO-GB01441.

07-MAY-1999; 08-MAY-1998;

18-NOV-1999

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This sequence represents the mutated CH2 molecule Gldeltaac, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule.

CC comprises: (a) a binding domain capable of binding a target molecule; and effector domain that is homologous to all or part of a constant comain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FogammaRilb C causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule or, an antibody, to the target of binding of a second binding molecule, e.g. an antibody, to the target consecue. The binding molecule is useful for the treatment of phagocytosis). The binding molecule is useful for the treatment of crejection, autoimmunity (e.g. vascullitis, autoimmune haemolytic anaemia, cutoimmune thrombocytopaenia and arthritis), alloimmunity and chrombocytopaenia and arthritis), alloimmunity (e.g. foetal/neonatal alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN (e.g. foetal/neonatal alloimmune thrombocytopaenia, asthma and cervonary artery occlusion). The binding molecules do not activate of properties have been retained. The polypeptides do not contain of groperties have been retained. The polypeptides do not contain on human amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind protein A, which is consistent contain a being able to cross the human placenta through interaction with FCRn channel FCRn and a processed to the contain and the contain and and are therefore likely to have reduced immunogenicity.
                                                         Immunoglobulin-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable
                                                                                                                                                                                            Claim 12; Fig 17; 81pp; English.
                                                                                                                                   immunoglobulin properties -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (neonatal Fc receptor).
WPI; 2000-039075/03.
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110 AA; Seguence

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ó;
                               Gaps
                                                   1 APPVAGGPSVFLFPPRPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                ;
0
98.1%; Score 576; DB 21; Length 110; 99.1%; Pred. No. 3.4e-52; 1ve 0; Mismatches 1; Indels
                                                                                                    61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                   Matches 109; Conservative
             Similarity
 Query Match
             Best Local
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AAY54996 standard; protein; 109 AA. Mutated CH2 sequence Gldeltaab. 17-FEB-2000 (first entry) AAY54996; AAY54996 RESULT 

Binding molecule; CHZ sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation, mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-va-host disease; organ transplant rejection; alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; sickle cell anaemia; coronary artery occlusion.

Synthetic.

W09958572-A1.

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This sequence represents the mutated CH2 molecule Gldeltaab, and is a binding molecule of the invention. The recombinant binding molecule of the invention. The recombinant binding molecule of scapable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: (a) a binding domain capable of binding a target molecule; and comprises: (a) a binding domain capable of binding a target molecule; and domain of a human immunoglobulin G (igG) heavy chain. The binding constant domain of a human immunoglobulin G (igG) heavy chain. The binding molecule causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding of a second binding molecule, e.g. an antibody, to the target molecule. The binding molecule is useful for the treatment of carafter disease, organ transplant rejection, bone-marrow transplant rejection, autoimmune thrombocytopaenia and arthritis, autoimmune thrombocytopaenia and arthritis, autoimmune thrombocytopaenia and arthritis, autoimmune caute inflammatory diseases (e.g. Crohn's, HDN (e.g. total/neonatal alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN (e.g. trigger cytotoxis) foetalis), The binding molecules do not activate complement or trigger cytotoxia, activities through FogammaR and desirable complement or trigger cytotoxia, and compared and arthribite complement or trigger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Igg properties have been retained. The polypeptides do not contain mon-numan amino acids, and are therefore likely to have reduced immunogenicity. Further, they still lond protein A, which is consistent with being able to cross the human placenta through interaction with FcRn
                                                                                                                                                                                                                                                                                    Immunoglobulin-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody; humanised; variable region; heavy chain; light chain; interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.2%; Score 570.5; DB 2
99.1%; Pred. No. 1.3e-51;
iive 0; Mismatches 0
                                                                                                                                                    (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                   Williamson LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW85689 standard; Protein; 468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D9D10 heavy chain fusion protein.
                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 17; 81pp; English.
                                                                                                                                                                                                                                                                                                                                   immunoglobulin properties -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neonatal Fc receptor).
                                                                                                                                                                                                   Armour KL, Clark MR,
                                                                                                                                                                                                                                             WPI; 2000-039075/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1999
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW85689;
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AAW85689
Dp
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New antibodies which bind and neutralise interferon-gamma (IFN gamma) can be used as a medicant, for preventing or treating septic shock, cachevia, immune diseases including multiple sclerosis and Crohn's disease and skin discoders including bullous, and Crohn's disease and skin discoders including bullous.

CC inflammatory and neoplastic dermatoses. The antibody is selected from a single chain antibody (ScFV), a chimeric antibody or diabody comprising the humanised variable domain of the monoclonal mouse anti-IFN gamma antibody 09D10; a multivalent antibody or a ruminant comprising the antibody 09D10; a multivalent antibody or a ruminant articody. The antibody of selected antibody or antibody were constructed. The light chain comprised cDNA encoding the mouse D9D10 alight chain fusion proteins of the humanised D9D10 light chain leader sequence. The humanised D9D10 light chain leader sequence constructed of humanised D9D10 light chain leader sequence constant domain in which the Clq-complement comprised cDNA encoding the mouse D9D10 light chain leader sequence. The manised D9D10 light chain leader sequence. This was then subsequently amplified using two primers (AAX08585-88) were used to construct the D9D10 light chain leader sequence. This was then subsequently amplified using two primers (AAX08594) and then cloned into pGEM-T-VHH using two fragments had a base pair overlap and were fused together using compensate NaX08593, AAX08594) and then cloned into pGEM-T to give with two primers (AAX08594) and then cloned into pGEM-T to give with two primers (AAX08594) and then cloned into pGEM-T to give
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with two primers (AAX08595, AAX08596) and cloned into pGEM-T to give pGEM-TCh. Two separate PCR amplifications were then performed using pGEM-T-Ch as a template. The primers used were AAX08599, AAX08599 to generate PCR-VIII fragment and AAX08597, AAX08600 to generate PCR-IX fragment. These were then overlapped and fused using primers AAX08599, AAX08600 and the resulting PCR-X fragment inserted into pGEMLGrVHh to generate the complete heavy chain fusion DNA in a vector designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New engineered antibodies which bind and neutralise interferon-gamma - useful for prevention and treatment of septic shock, cachexia, immune diseases and skin disorders
                                                                                                                                                                                                                           /note= "Humanised heavy chain variable domain of D9D10"
                                                                                                                                                                                                                                                                                            'note= "Human IgG1 heavy chain constant domain"
immume disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv; multivalent; ruminant.
                                                                                                                                                                               /note= "D9D10 light chain signal peptide"
                                                                                                                                                                                                                                                                                                                                 /note- "Leu added by cloning strategy
                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 9; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98EP-0870139.
97EP-0870122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-EP05165
                                                                                                                                                                                                                                                                      138..467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-180969/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sablon E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX08631
                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                          WO9909055-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1999
                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buyse M,
                                                                                                                                                                  Peptide
                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                 Key
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pGEMhD9D10H. For a description of the construction of the light chain fusion cDNA see GENESEQ records AAX08573-X08584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "This mutation decreases the affinity of the Fc portion for complement"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "This mutation decreases the affinity of the Fc
                                                                                                                                                                                                                                                                                                                                                    FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein; inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Human_IgG1_Fc_region
/note= "Contains hinge region and domains CH2 and CH3"
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22..257
/label= FGF-R1_extracellular_domain
/note= "The Ig I segment and acid box are deleted"
                                                                                                                      1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                 ö
                                                                       Length 468;
                                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                              Human FGF-RI Extracellular domain-Ig Fc fusion protein 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     portion for Fc receptors"
                                                                       Score 562; DB 20;
Pred. No. 5.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- FGF-R1_signal_peptide
                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig_III_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Ig_II_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                     AAY97175 standard; Protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= L276E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= P376S
                                                                       95.7%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2000; 2000WO-US03166.
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                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157..222
/label= I
                                                                                              Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258..488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR ) CHIRON CORP.
                                                                         Query Match
Best Local Similarity
                                     468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA52132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200046380-A2
рсемьрэр10н.
                                                                                                                                                                                                                                                                                                     04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-2000.
                                                                                                                                                                                                                                                                               AAY97175;
                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
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                                                                                                                                                                                                                                           AAY97175
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Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin (GG (Ig)) regement fused to a heterologous oligomerization domain that comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 region, or light chain of an immunoglobulin molecule, or a peptide with a comprise rmotif. The Ig I segment is not necessary for binding of acidic FGF and basic FGF (PFGF). The Ig I deletion further increases the cord affinity for aFGF and heparin, protects the core of the molecule from new fusion polypeptides are better FGF inhibitors than FGF-R monomer or proteins. The FGF-R inhibitors than FGF-R monomer CC proteins. The FGF-R for fusion dimmers are active as FGF antagonists at subnanomolar concentrations and were 20-fold more potent than the FGF-R monomer protein as competitors of bEGF binding to immobilized FGF-R fusion constructs are useful to treat FGF-, angiogenesis, or CGF-R-mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung, rectal, testis and cervical tumouris), meovascular smooth muscle cells (e.g. postangioplasty and postatherectomy restenosis).
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                          for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization domain treating FGF-, anglogenesis-, or FGF receptor-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..21
/label= FGF-R1_signal_peptide
22..257
/label= FGF-R1 extracellular_domain
/note= "The Ig I segment and acid box are deleted"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 562; DB 21;
Pred. No. 5.9e-50;
2; Mismatches 3;
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/label= Human_IgGl_Fc_region
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/label-_Ig_III_segment
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/label= Ig_II_segment
                                                                Claim 14; Page 68-69; 70pp; English.
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95.5%;
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les 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin (CG receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin CC receptor (Ig) I segment for a heterologous oligomerization domain that comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 region, or light chain of an immunoglobulin molecule, or a peptide with a comprise inotif. The Ig I segment is not necessary for binding of a cidic FGF and basic FGF (BFGF). The Ig I deletion further increases the core affinity for aFGF und heparin, protects the core of the molecule from the fusion polypeptides are better FGF inhibitors than FGF-R monomer content only peptides are better FGF inhibitors than FGF-R monomer content as competitors of BFGF inhibitors than the FGF-R monomer constructs are useful to treat FGF-, anglogenesis-, or fusion diamers are active as FGF antagonists at subnanomolar constructs are useful to treat FGF-, anglogenesis-, or clung, rectal, testis and cervical tumnurigenesis (e.g. bladder, breast, clung, rectal, testis and cervical tumnurs), neovascularization (e.g. diabetic retinopathy, neovascular smooth muscle cells (e.g. postangioplasty and postatherectomy restenosis).
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/note= "Contains hinge region and domains CH2 and CH3"
285
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                                                                                                                                /note= "This mutation decreases the affinity of the portion for complement"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APPVAGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.7%; Score 562; DB 21; Length 497; 95.5%; Pred. No. 6.1e-50; tive 2; Mismatches 3; Indels
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                                                                                       Misc-difference 385
/label= P385S
                                       /label= L285E
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Matches 105; Conservative
                                                              /note=
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                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-514961/46.
                     Misc-difference
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receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin

(IG) I segment fused to a heterologous oligomerization domain that

comprises an immunoglobulin Fc region, hinge region, CHJ, CHJ, CHJ, CHJ, CHJ,

region, or light chain of an immunoglobulin molecule, or a peptide with a

leucine zipper motif; The Ig I segment is not necessary for binding of

eucidic FGF and basic FGF (bFGF). The Ig I deletion further increases the

coidic FGF and basic FGF (bFGF). The Ig I deletion further increases the

affinity for aFGF and heparin, protects the core of the molecule from

proteolysis, and abrogates the heparin requirement for aFGF binding. The

new fusion polypeptides are better FGF inhibitors than FGF-R monomer

proteins. The FGFR-IG FC fusion dimers are active as FGF antagonists at

submanomolar concentrations and were 20-fold more potent than the FGF-R

monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The

fusion constructs are useful to treat FGF-, anglogenesis, or

fusion constructs are useful to treat FGF-, anglogenesis, or

FGF-R-mediated disorders, such as tumourigenesis (e.g. bladder, breast,
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                                                                                                                                FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein; inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative.
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/label= Human_IgGl_Fc_region
/note= "Contains hinge region and domains CH2 and CH3"
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                                                                   Human FGF-RI Extracellular domain-Ig Fc fusion protein 4.
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/label= FGF-R1_extracellular_domain
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/label= FGF-R1_signal_peptide
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/label= Acid_box_segment
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(first entry)
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/label= L
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04-DEC-2000
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lung, rectal, testis and cervical tumours), neovascularization (e.g. diabetic retinopathy, neovascular glaucoma, wound healing and corneal scarring) and hyper-proliferation of vascular smooth muscle cells (e.g. postangioplasty and postatherectomy restenosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody; humanised; variable region; heavy chain; light chain; interferon gamma; IFN; treatment; prevention; septic shock; cachexia; immune disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv; multivalent; ruminant.
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- Mouse_D9D10_light_chain_signal_peptide
21..137
/note- "Humanised heavy chain variable domain of
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                     Length 525;
                                                                                                                                                                                                                                                                                                                                                                    61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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/note= "Human 1gG1 heavy chain constant
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                                                                                                                                                                                   Score 562; DB 21;
Pred. No. 6.5e-50;
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/label= Humanised)_D9D10_ScFv
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/label- Gly(3)Ser_linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW85692 standard; Protein; 711 AA
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                                                                                                                                                                              95.7%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-EP05165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MoTAbII fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-180969/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buyse M, Sablon E;
                                                                                                                                                                                                           Similarity
                                                                                                                   525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAW85692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9909055-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .8-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW85692;
                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Peptide
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                                      gamma) can be used as a medicant, for preventing or treating septic shock, cachexia, immune diseases including bullious and crohn's disease and skin disorders including bullious, inflammatory and neoplastic dermatoses. The antibody is selected from a single chain antibody (scFv), a chimeric antibody or diabody anti-IFN gamma antibody 99910; a multivalent antibody; or a ruminant antibody. The antibodies are also useful for determining IFN
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                       ZTNFR-6; tumour necrosis factor receptor-6; human; IgGl; Fc region;
cell maturation; bone cell regulation; mutant.
                            New antibodies which bind and neutralise interferon-gamma (IFN
                                                                                                                                                                                                      .;
0
                                                                                                                                                                            Query Match 95.7%; Score 562; DB 20; Length 711; Best Local Similarity 95.5%; Pred. No. 9.4e-50; Matches 105; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                             61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                        'note= "Leu in native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Leu in native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Ala in native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Pro in native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Gly in native
           Disclosure; Fig 20; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    AAY05688 standard; Protein; 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matthews SM;
                                                                                                                                                                                                                                                                                                                                                                                                  Modified human IgG Fc sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US18364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0923725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0057608
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                          gamma levels in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Farrah TM, Gross JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-205190/17.
N-PSDB; AAX25272.
                                                                                                                                               711 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                              19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-1997;
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                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                         AAY05688;
                                                                                                                                                                                                                                                                                                                           AAY05688
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a modified human IgG1 Fc region in which the FCGRI binding site has been mutated from Leu-Leu-Gly-Gly Lo Ala-Glu-Glu-Ala in order to reduce FCRI binding, and residues Ala-134 and Pro-135 have been altered to Ser-134 and Ser-135 to reduce complement Clq binding and/or complement fixation. The mutations were introduced into the native FC DNA sequence by PCR-mediated mutagenesis (see also AAX5272). The construct was utilised in the preparation of ZTNFR-6-1g fusion vectors. Soluble ZTNFR-6 (see AAVD5679) was expressed in BHK 570 mammalian cells and also in baculovirus-infected Spodoptera frugiperda sf9 insect cells. ZTNFR-6 is a novel human tumour necrosis factor receptor. ZTNFR-6 puppetides are useful for promoting cellular maturation and hone cell remulation.
secreted or membrane bound tumor necrosis factor receptor 'R-6 - useful for detecting a genetic abnormality in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZINFR-5; tumour necrosis factor receptor; INFR; human; cell maturation; bone cell regulation; IgG1; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 Preegynstyrvvsvltvlhqdwlngkeykckvsnkalpssiektiskak 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel tumour necrosis factor receptor ZTNFR5 - useful for regulating maturation of TNF-ligand bearing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     95.1%; Score 558; DB 20; 95.5%; Pred. No. 6.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                     Example 4; Page 138-139; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 90-92; 109pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified human 1gG1 Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US15072.
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                                                                                                                                                                                                                                                                                                                           and bone cell regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion protein; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-132245/11.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                               251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX07232
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97756;
                   ZTNFR-6
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Example 6; Page 170-172; 175pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
This polypeptide comprises a modified human IgG1 Fc region. IgFc cDNA was amplified from a human foetal liver library by PCR (see AAX072031). PCR was also used to introduce mutations within the Fc region to reduce FcgRI binding, and to introduce A1345 and P1355 mutations to reduce complement Clq binding and/or complement fixation (see also AAX07232). Mammalian and baculovirus expression vectors for soluble mutated IgFc were prepared, and used to construct ZTNRFR-5-mutated IgFc were prepared, and used to construct ZTNRFR-5-mutated IgFc were prepared, and used to soluble mutation temour necrosis factor receptor ZTNFR-5. ZTNFR-5 polypeptides and nucleic acids (see AAX07256) can be used to screen for ligands, agonists and antagonists of ZTNFR-5. The polypeptides can be used in bone cell regulation and to regulate the maturation of TNF ligand-bearing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGGESVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 apeaegapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktk 94
                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                        Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          renal artery stenosis; occlusion; cholesterol; renal emboli
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                 Score 558; DB 20;
Pred. No. 6.9e-50;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of the human Fc region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB07541 standard; Protein; 251
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.5%;
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-0CT-2000
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                                                                                                                                                                                                                                                                                              Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin; antiinflammatory; antipsoriatic; antiasthmatic; antibacterial; human; dermatological; antiulcer; antagonist.
                                                                                                                                                A human Fc region polypeptide, which is used in the course of the invention. The specification describes extracellular domains of BR43x2 (an isoform of the transmembrane activator and CAML-interactor (TACI) receptor). TACI or BCMA (a related B cell protein). These contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. They may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity and BK43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated interleukin 20 soluble receptor comprising two polypeptide subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL-20RA-Ig gammal constant region fusion protein extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                         DB 22; Length 559;
                                                                                                                                                                                                                                                                                                                                                                 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                              Score 558; DB 22; Length 5:
Pred. No. 1.8e-49;
0; Mismatches 5; Indels
treating inflammatory diseases such as psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- Linker_peptide
265..594
/label- Immunoglobulin_heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36..594
/label- Mature_fusion_protein
36..249
/label- Extracellular_domain
                      Claim 8; Page 110-112; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...33
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU04062 standard; Protein; 594 AA.
                                                                                                                                                                                                                                                                    Query Match 95.1%;
Best Local Similarity 95.5%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-2600; 2000WO-US35305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250..264
                                                                                                                                                                                                                                     559 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200146261-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2001.
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU04062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                         403
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU04062
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Treating interleukin-20 induced inflammation in a mammal, such as adult respiratory disease, eczema, psoriasis, contact dermatitis, multiple organ failure and septic shock, involves administering IL-20 antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the Human interleukin-20 receptor A, IL-20RA/ inmunoglobulin kappa heavy chain fusion protein, consisting of a signal peptide from tissue plasminogen activator; tpa, amino acids 30-243 of IL-20RA (extracellular domain) and human immunoglobulin kappa heavy chain. The invention relates to treating a mammal afflicted with a disease in which an interleukin-20 (IL-20) polypeptide plays a role, involves administering antagonist of IL-20 polypeptide to the individual. The method is useful for treating psoriasis, eczema, atopic dermatitis, contact dermatitis, adult respiratory disease, asthma, bronchitis and pneumonia and is also useful for treating multiple organ failure, inflammatory lung injury, septic shock, bacterial pneumonia, inflammatory bowel disease, rheumatoid arthritis, ulcerative colitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin; antiinflammatory; antipsoriatic; antiasthmatic; antibacterial; human; dermatological; antiulcer; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelly JD;
, Chandrasekher JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APPVAGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IL-20RA-Ig gamma 1 constant.region fusion protein.
                                                                                                                                          Madden KL, Ko
Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 558; DB 22
Pred. No. 2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 75-76; 117pp; English.
                                                                                                                                          Wenfeng X,
Eagan MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB85274 standard; Protein; 594 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.1%;
95.5%;
23-DEC-1999; 99US-0470898.
22-JUN-2000; 2000US-0213341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-2000; 2000WO-US35307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0471774.
                                                                                                                                     Foster DC, We
Blumberg H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.57
Matches 105; Conservative
                                                                                (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                             WPI; 2001-418045/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       594 AA;
                                                                                                                                                                                                                                                                          N-PSDB; AAS07649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200146232-A2.
                                                                                                                                     Thompson P,
Sprecher CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUN-2001
                                                                                                                                                                                            Novak JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB85274;
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Ы Д Rixon MW,

Foster

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The sequences given in AAR41682-85 are encoded by the expression vector,
                                                                                                                                                                                              In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17. The inventor's propose eliminating these allotypes by amino acid changes to agree with the sequences of igG2, IgG3 and IgG4. None of the allotype sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes" should be suitable for therapeutic use in all patients. See AAR27678-R27681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                 Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                            Humanised antibodies having modified allotypic determinant useful for matching allotypes in therapy with decreased likelihood of causing undesirable immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Score 557; DB 13;
Pred. No. 3.2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 11K; 151pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Undefined ORF2 encoded by pAH4602.
                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR41684 standard; Protein; 110
                                                                                                                                                                                                                                                                                                                                                                                               Query Match

Best Local Similarity 94.5%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0800458.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                           Disclosure; Fig 4c; 57pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALKE-) ALKERMES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-196742/24.
N-PSDB; AAQ43844.
                                       WPI; 1992-349162/42.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9310819-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
  Clark MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR41684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR41684
ID AAR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                            The invention relates to an interleukin 20 (IL-20) soluble receptor comprising two polypeptide subunits IL-2DRA (formerly known as EcytoR7) and IL-2DRB (formerly known as DIRSI). The two subunits are preferably linked together. In one embodiment, one subunit is fused to the constant region of the light chain of an immunoglobulin, and the other subunit is fused to constant region of the heavy chain of an immunoglobulin. The light chain and the heavy chain are connected via a dissiphide bond. The soluble receptor can be used to down-regulate IL-20 and thus treat inflammatory diseases such as psorthasis, inflammatory lung injury such as asthma or bronchitis, adult respiratory disease (ARD), septic shock, multiple organ failure, bacterial pneumonia, eczema, atopic and contact Crohn's disease. The present sequence represents DNA sequence of a construct containing the extracellular domain of IL-20RA fused to a
                                                                                                                                                                                              Isolated interleukin 20 soluble receptor comprising two polypeptide subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus treating inflammatory diseases such as psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                Brandt CS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.1%; Score 558; DB 22; Length 594; 95.5%; Pred. No. 2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                Sprecher CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isoallotype; IgG1 Glm(1,2,17); anti-allotype response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutated human immunoglobulin gamma 1 constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                              Kelly JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunoglobulin IgG1 CH2 region.
                                                                                                                                                                                                                                                                             Claim 8; Page 81-82; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR27680 standard; Protein; 110 AA
                                                                            n KL, Ke
Fox BA;
22-JUN-2000; 2000US-0213416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 105; Conservative
                                     (ZYMO ) ZYMOGENETICS INC
                                                                            Xu W, Madde
Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LYNX-) LYNXVALE LTD.
                                                                                                                                      2001-398320/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       594 AA;
                                                                                                                                                         N-PSDB; AAH22821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAR-1993
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Sequence

Query Match

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AAR27680

AAR27680

RESULT

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Gaps

chain variable region (VH) of the antibody 128.1, an amplcillin resistance gene and a histidine (histidinel) selection marker.

resistance gene and a histidine (histidinel) selection marker.

Transcription of the VH gene is from the VH promoter of the murine chiancer and the human gammal constant region (CH). The VH region of pAH4274. This was achieved by digesting the plasmid and the product with EcoRV and Nhel. The VH gene was inserted in-frame with the human gammal characterial and the plasmid and the product with EcoRV and Nhel. The VH gene was inserted in-frame with the human gammal CH region CH at the 3' end of the VH-J region by means of a Nhel site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, all and antibody. diagnostic methods 

Seguence

Query Match
94.9%; Score 557; DB 14; Length 110;
Best Local Similarity 94.5%; Pred. No. 3.2e-50;
Matches 104; Conservative 2; Mismatches 4; Indels (

; 0 Gaps 1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60

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Search completed: June 21, 2002, 08:36:06 Job time: 320 sec

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GC1_HUMAN
P01857;
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mus musculu
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                                                                                                                                                                                                                                                                                                                                                                                                                                      oryctolagus
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                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gorilla
                                                                                                                                                                                                                                                                                                                                                                                                  pomod
                                                                                                                                                                                                                                                                                                                                                                                                        homo
                                                                                                                                                                                                                                                                                                                                                     mus
                                                                                                                                                                                                                                      Description
                                                                         APELLGGPSVFLFPPKPKDT......CKVSNKALPAPIEKTISKAK
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                                    June 21, 2002, 09:00:23; Search time 48.19 Seconds
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| 122                     | 121<br>115.5                             | 115.5          | 113.5      | 112.5     | 110.5      | 110.5        | 110.3              |
| 34<br>35                | 36<br>37                                 | 38<br>30<br>30 | 40         | 42        | 43         | 44           | 4,<br>U            |

## ALIGNMENTS

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SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
MEDLINE-71064024; PubMed-5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
Blochemistry 9:3161-3170(1970).
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MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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The
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MEDLINE-77070269; PubMed-826475;
Ponstingl H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymcir peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The covalent structure of a human gamma G-immunoglobulin. 8. acid sequence of heavy-chain cyanogen bromide fragments H5-H7 Biochemistry 9:3171-3181(1970).
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Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 136-329 (EU).
MEDLINE-71064025; PubMed-5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
                                                         11-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
330 AA
PRT;
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STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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330 AA;
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    GC4_HUMAN
P01861;
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                                                                                                                                   Deisenhofer J.;
"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus Biochemistry 20:2361-2370(1981).

-I MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.

-I MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

-I MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
                                             Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal igd1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                  MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
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/FIId=VAR_003886.
D -> E (IN GIM(NON-1) MARKER).
/FIId=VAR_003887.
L -> M (IN GIM(NON-1) MARKER).
/FIId=VAR_003888.
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INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
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REMOVED POST-TRANSLATIONALLY.
                                                                                                                X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; Pubmed=7236608;
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CH2.
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                           DISULFIDE BONDS.
MEDLINE-77070267; PubMed-1002129;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_llke.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 2.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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PDB; 1FC1; 15-JUL-92.
PDB; 1FC2; 15-JUL-92.
MIM; 147100; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                        Length 330;
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MEDILINE=83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 g
                                                                                                                    Indels
36106 MW; 3770EE106C2FA33D CRC64;
                                                                   100.0%; Score 586; DB 1;
100.0%; Pred. No. 5.9e-52;
ive 0; Mismatches 0;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ig gamma-4 chain C region.
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SEQUENCE OF 1-30 AND 81-326.
MEDLINE-70207560; PubMed-4192699;
                                                                Query Match
Best Local Similarity 100.0
Matches 110; Conservative
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 between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Michaelsen T.E., Frangione B., Franklin E.C.;
Primary structure of the 'hinge' region of human 1gG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1g gamma-3 chain C region (Heavy chain disease protein) (HDC)
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INTERCHAIN (WITH A LIGHT CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 19:4304-4308(1980).
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InterPro; IPR003597; Ig_Cl.
InterPro; IPR003597; Ig_Cl.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGCl; 2.
PROSITE; PS00290; IG_MHC; 2.
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327 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CHI REGION.
-!- MISCELLANEOUS: DISEASE PROTEIN LUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAMMA-3 HEAVY CHAINS.
-!- MISCELLANEOUS: DISEASE PROTEIN OWN MAY REPRESENT AN ALLELIC FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR ANOTHER GAMMA CHAIN SUBCLASS.
MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE EIDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
                                                                                                                                                                    SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).

MEDLINE-82447835; PubMed-6608565;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
Franklin E.C., Hood L., Buxbaum J.N.;
Gamma Heavy chalt disease in man: cDNA sequence supports partial
gene deletion model.";
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

-!- SUBUNIT: DIMERE LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFEDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
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[3]
REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
MEDLINE-77021516; PubMed-823945;
Wolfenstein-Todel C., Frangione B., Prelli F., Franklin B.C.;
"The amino acid sequence of 'heavy chain disease' protein ZUC.
Structure of the Fc fragment of immunoglobulin G3.";
Biochem. Blophys. Res. Commun. 71:907-914(1976).
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CARBOHYD
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PIR; A02148; G2HU.
HSSP; P01857; 1FC1.
MIM; 147110; -.
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MEDLINE-8423992; bubMed-6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
                                                                                                                                                                                                                             14 APELLGGPSVFLFPPKPKDTLMISTTPEVTCVVVDVSHEDPEVQFKWYVDGVQVHNAKTK 133
                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE OF 2-326 FROM N.A.
MEDILINE-8131976511; PubMed-6804948;
Ellison J.W., Hood L.E.;
Linkage and sequence homology of two human immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T., "Structure of human immunoglobulin gamma genes: Implications for evolution of a gene family."; cell 29:671-679(1982).
                                                                                                                                                                                                   ;
.. LLINEL (GLCNAC. . .).

REMOVED POST-TRANSLATIONALLY.

QV -> EB (IN ZUC).

/FTIG=VAR_003890.

P -> L (IN OMM).

/FTIG=VAR_003891.

F -> Y (IN OMM).

/FTIG=VAR_003892.

T -> A (IN OMM).
                                                                                                                                                                                                                                                                   134 PREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183
                                                                                                                                                                                                                                                         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                               Score 548; DB 1; Length 290;
Pred. No. 3.5e-48;
7; Mismatches 2; Indels
                                                                                                                                  F -> Y (IN OMM).
/FTId=VAR_003896.
E69CBC95705B2F46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
                                                                           T -> A (IN OMM).
/FTId=VAR_003893.
                                                                                                     FTIG=VAR_003894
                                                                                                                MISSING (IN ZUC)./FTId=VAR_003895.
                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
1G gamma-2 chain C region.
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MEDLINE-81007873; PubMed-6774012;
Wang A.-C., Tung E., Fudenberg H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 99-177 AND 310-326 FROM
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MEDLINE-83001943; PubMed-6811139;
                                                                                                                                                     MM;
                                                                                                                                                                               Query Match 93.5%;
Best Local Similarity 91.8%;
Matches 101; Conservative
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P01859;
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           MOD_RES
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MEDILINE=72033500; PubMed=4940472;
Milstein C., Frangione B.;
Histein C., Frangione B.;
Bisulphide bridges of the heavy chain of human immunoglobulin G2.";
Biochem. J. 121:217-225(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G., "Characterization of the two unique human anti-flavin monoclonal
                                                                                                                SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).

WEDLINE-BROO1377, Pubmed-113060,

Connell G.E., Parr D.M., Hoffmann T.;

"The amino acid sequences of the three heavy chain constant region
                                                                                                                                                                                                                                                                                     [6]
SEQUENCE OF 238-275 (ZIE).
SEQUENCE OF 14419; PubMed=118920;
Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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"The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications."; J. Immunol. 125:1048-1054(1980).
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                                                                                                                                                                                                                                   domains of a human IgG2 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEVISIONS TO 25; 59; 60 AND 264-268 (ZIE). Hofmann T., Parr D.M.; Submitted (MAR-1980) to the PIR data bank.
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HINGE.
CH2.
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MEDLINE=95255598; Pubmed=7737190;
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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Brueggemann M.;
"Pvolution of the rat immunoglobulin gamma heavy-chain gene family.";
"Pvolution of the rat immunoglobulin gamma heavy-chain gene family.";
PIR 187018. PS0018. PS0018.
INTERPROSIPTION OF TABB.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600, Ig_like.
PEm; PF00017, ig; 3.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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       AT OR NEAR THE COMPLEMENT-BINDING SITE.

REMOVED POST-TRANSLATIONALLY (PROBABLE)

S -> A (IN MYELOMA PROTEINS TIL & ZIE).

FITA-VAR_003889.

C -> S (IN REF. 3).

8310878C6878CF9C CRC64;
                                                                                                                5 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 64
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                            Score 534; DB 1; Length 326; Pred. No. 1e-46;
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                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FUL-1999 (Rel. 38, Last annotation update)
19 gamma-2B chain C_region.
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                                                                                               5; Mismatches
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92.5%;
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SMART; SM00407; IG_1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                    35884
                                                                            Query Match
Best Local Similarity 92.5³
Matches 98; Conservative
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333 AA;
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es 80; Conserv
                                                     326 AA;
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SEQUENCE FROM N.A.
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                                          CONFLICT
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P20761;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pratt D.M., Mole L.E.; "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype."; Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- MISCELLANBOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKERS.
                                                                                                                                                                                                      Oryccolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [5] SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
Hill Rillander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-70110015; PubMed-5461106; Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.; Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 88-266 FROM N.A.
MEDLINE-83299917: PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit IgG: isolation of a cDNA encoding
heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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T -> A (IN E15 MARKER).
N -> E (IN REF. 2).

      Immunoglobulin domain; Immunoglobulin C region.

      NON_TER
      1

      VARIANT
      104
      T -> M (IN D11 MAR)

      VARIANT
      185
      T -> A (IN B15 MAR)

      CONFLICT
      48
      48
      N -> E (IN REF. 2)

                                                                                                       21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
323 AA.
       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE OF 1-128.
MEDLINE-76135469; PubMed-1243651;
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-84030930; PubMed-6313520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenetics 18:387-397(1983).
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                                                                  (Rel. 01, Created)
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HSSP; P01857; IFC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 1g; 3. SMART; SM00407; IGc1; 2. PROSITE; PS00290; IG_MHC; 1.
       STANDARD;
                                                                                                                                                                            Ig gamma chain C region.
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                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F-I haplotype.
                                                                     21-JUL-1986
21-JUL-1986
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PRT;
                                                     DISULFIDE BONDS.
MEDLINE=71058474; Pubmed=4922544;
                   lochemistry 13:4804-4811(1974).
                                                                                                                                                                        PIR; A02151; G2CP.
HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 3.
SMART; SM00410; ig_like; 1.
SMART; SM00407; ig_like; 1.
PROSITE; PS00290; ig_MHC; 1.
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105
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178
248
329 AA;
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P22436:
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the carboxyl-terminal
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"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                2 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-75036072; Pubmed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 227-311.
Macd-4609467;
Trischmann T.M., Cebra J.J.;
Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia
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                                                                                                                                                                                                                                                                              Score 450; DB 1; Length 323;
Pred. No. 3e-38;
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2).
AND 4).
                                                     AND 5).
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"Structure of heavy chain from strain 13 guinea immunoglobulin-(52). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
 REF.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 AA
                                                                                                                                                                                                                                                                                                                12; Mismatches
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MEDLINE-71058486; Pubmed-5538616;
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Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                            35404 MW;
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75.2%;
                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                          323 AA;
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P01862;
CONFLICT
CON
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Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin."; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin."; Biochemistry 10:26-31(1971).
--- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED GUINEA PIGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 PENLGGPSVFIFPPRKRDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKP 172
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of the murine \lg 63 constant region gene."; \rm EMBO~J.~3:2041-2046(1984).
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HEAVY CHAIN).
HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin domain; Immunoglobulin C region; Glycoprotein. NoN_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.3%; Score 447; DB 1; Lv
Best Local Similarity 76.1%; Pred. No. 6.2e-38;
Matches 83; Conservative 10; Mismatches 16;
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01-AUG-1991 (Rel. 19, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region, secreted form.
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InterPro; IPR003006;
InterPro; IPR003597;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
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0
                     HISSP, PO1857; IFCI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003609; Ig_like.
Pfam; PF00047; Ig. 3.
SWART; SW00410; IG_like; 1.
SWART; SW00407; IG_like; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                      Length 329;
                                                                                                                                                                                                                     74.1%; Score 434; DB 1; Length 32 72.9%; Pred. No. 1.3e-36; ive 14; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                            64 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                        176 AQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPK 222
                                                                                                                                                     98 113 HINGE.
114 223 CH2.
224 327 CH3.
329 AA; 36228 MW; F45827174182BAD6 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma -3 chain C region, membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                         398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 11:6775-6785(1983).
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HINGE.
CH2.
CH3.
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   -; NOT_ANNOTATED_CDS
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EMBL; V01526; CAA24767.1; ALT_SEQ.
                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 78; Conserva
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PIR; A02155; G3MSM.
HSSP; P01857; 1FC1.
EMBL; 100451; -; N
PIR; B02156; G3MSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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P03987;
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SEQUENCE
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-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE, FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
SMART; SM0047; Ig_like.
SMART; SM00410; Ig_like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; Ig_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.1%; Score 434; DB 1; Length 398; 72.9%; Pred. No. 1.6e-36; Live 14; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 AQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPK 222
                                                                                                                                                                                                                                                                                                                                                                                                                      E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, B allele.
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POTENTIAL.
CYTOPLASMIC
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CH2.
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MEDLINE=82037777; PubMed=6794027;
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Matches 78; Conservative
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GC1M_MOUSE
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MEDILIBE-80012837; PubMed-113776;
ROGETS J., Clarke P., Salaer W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                               1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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MEDLINE-80202559; PubMed-6769752;
Obata M., Yamawaki-Rataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evolution of immunoglobulin subclasses. Primary structure of a
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                                                                                                                                                                                                                                                                                                                             Length 335;
                                                                                                                                                                                                                                                                                                                        70.6%; Score 414; DB 1; Length 33 67.3%; Pred. No. 1.4e-34; Indels iive 19; Mismatches 17; Indels
                                                                                                                                                                                                                                                            335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
                                                                                                                                                                                              PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AA.
EMBL, J00479; -; NOT_ANNOTATED_CDS.
PTR: A02153; G2MSAB.
HSSP, P01857; 1FC1.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003507; Ig_Like.
Pfan, PF0047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
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J. Biol. Chem. 253:6068-6075(1978).
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MEDLINE=73008889; PubMed=5073237;
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                                                                                                                                                                                                                                                                                                                                                                  74; Conservative
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Cell 18:559-568(1979)
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Best Local Similarity
Matches 74; Conserv
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TAXID=10090;
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R EMBL; V00793; CAA24172.1; -.

R EMBL; V00793; CAA24172.1; -.

R EMBL; V00793; CAA24174.1; -.

R EMBL; V00793; CAA24176.1; -.

R EMBL; V00795; CAA24176.1; -.

R GJYCCSUILEDB; P01868; -.

R GJYCCSUILEDB; P01868; -.

R MGD; MGI:96446; Igh-4.

R InterPro: IPR003597; Ig_C1.

R Pfam; PF00047; Ig: 3.

R SMRAT; SM00407; IGC1, 2.

R PROSITE; PS00290; IG_MHC; 1.

R Immunoglobulin domain; Immunogl
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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74; Conservative
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358 3
                                             Best Local Similarity
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DISULFIDE BONDS
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                                                                                                                                                                        GCAA_MOUSE
DOMAIN
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                                   Query Match
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                                                                                                                                                                                                                                  Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.; "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                        "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";
                MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
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CHAIN).
CHAIN).
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CH2.
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                                                                             SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197626; PubMed-6804950;
                                                                                                                                                     SEQUENCE OF 323-366 FROM N.A. MEDLINE-82115295; PubMed=6799207;
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; V00793; CAA24172.1; -. EMBL; V00793; CAA24173.1; -. EMBL; V00793; CAA24174.1; -. PIR; B02159; GIMSM.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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324
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102
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Cell 18:559-568(1979)
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       SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                             gamma 2b chain genes
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MEDIINE-81076554; PubMed-6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chaln messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                   2 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
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"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                   'n
                                                                                                                                    Length 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 REEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 217
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CYTOPLASMIC (POTENTIAL).
4CC88343B7A1CE27 CRC64;
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                                                                                                                                       70.2%; Score 411.5; DB 1 67.9%; Pred. No. 2.9e-34;
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(Rel. 01, Last sequence update)
                                                                                                                                                                                                               19; Mismatches
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MEDLINE-81223894; PubMed-6787604;
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PIR; S00847; S00847.
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399 AA;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-8122190; PubMed=6283537;
MEDLINE-8122190; PubMed=6283537;
Mucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
Proc. Natl. Acad. Sci. U.S.A. 79:2623 PRODCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.

SEGMENT OF MU CHAINS.

ILLEANZOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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B84361C5445A6864 CRC64;
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15-UUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                              PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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                                                          HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003609; Ig_C1.
InterPro; IPR003600; Ig_1ike.
Pfam; PF00047; Ig; 3: SMART; SM00410; IG_1ike; 1.
SMART; SM00407; IG_1ike; 1.
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                                     EMBL; V00798; CAA24178.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Brueggemann E., Delmastro-Galfre P., Waldmann H., Calabi F.;
Sequence of a rat immunoglobulin gamma 2c heavy chain constant
region CDMA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
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4C38138BFAED3FF0 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
1g gamma-2C chain C region.
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                                                                               EMBL; J00471; AAB59661.1; ALT_INIT
                                                                                                                                  HSSP, P01857; IFCI...
MGD: MGI:96443; Igh-1.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003600; Ig_like.
Pfam; PF00407; Ig, 31.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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Best Local Similarity 66.4.
To 75, Conservative
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DR HSSP, P01857; 1FC1.

DR InterPro: IPR000306; 1g_MHC.

DR InterPro: IPR001306; 1g_MHC.

DR InterPro: IPR001306; 1g_Like.

DR Ffam; PF00047; 1g_3.3.

DR SWART; SW00407; 1g_3.3.

DR SWART; SW00410; 1G_Like; 1.

DR SWART; SW00410; 1G_Like; 1.

DR SWART; SW00410; 1G_Like; 1.

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"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer."; proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
EMBL: AF272774; AAK58686.1; SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FACTOR VII ACTIVE SITE MITANT IMMUNOCONUGATE.
Homo sapiens (Human).
Evkaryotis, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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100.0%; Pred. No. 1.8e-56;
iive 0; Mismatches 0;
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SEQUENCE FROM N.A.
MEDLINE=21477448; PubMed=11593034;
Hu Z., Garen A.;
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                                                                                                                                                        Query Match
Best Local Similarity 100.(
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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096ga6 homo sapien
096aa6 homo sapien
090544 ginglymosto
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Q95m34 equus cabal
Q9d814 mus musculu
Q971a4 mus musculu
Q991c4 mus musculu
Q99131 mus musculu
Q99125 mus musculu
Q99125 mus musculu
                                                                                                                               June 21, 2002, 08:59:30 ; Search time 176.89 Seconds (without alignments) 107.578 Million cell updates/sec
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                                                                                                                                                                                                                                                     1 APELLGGPSVFLFPPKPKDT.......CKVSNKALPAPIEKTISKAK 110
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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sp_unclassified:*
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sp_plant:*
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sp_virus:*
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Result

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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR152312, AD40243.1;
HSSP; PO1842; 7FAB.
InterPro; IPR003600; Ig_like.
InterPro; IPR003606; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
          Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                     Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 67.9%; Score 411.5; DB 11; Length 437; Similarity 67.9%; Pred. No. 2.3e-37; P4; Conservative 19; Mismatches 13; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9DED57A514475FBB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAMMAI HEAVY CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

70.6%; Score 414; DB 11;
Best Local Similarity 67.3%; Pred. No. 1.3e-37;
Matches 74; Conservative 19; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
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SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
SMART; SM00410; IGC1; 3.
SMART; SM00410; IGC1/1ke; 1.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 473 AA; 51699 MW; 9DED57P
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SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                     Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -. HSSP; PO1842; 7FAB.
MGD: MGI:96443; 19h-1.
InterPro; IPR003599; 1g.
InterPro; IPR003600; 1g_c1.
InterPro; IPR003600; 1g_like.
InterPro; IPR003600; 1g_like.
InterPro; IPR003595; 1g_v.
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                                                            Hayashizaki Y.;
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Matches 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagner B., Overesch G., Shoran A., Holmes M., Richards C., Leibold W., Radbruch A.; Capania Constant and Corganization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-119(1998).

EMBL: AJ300675; CAC44624.1; -.
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                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1 Similarity 78.2%; Pred. No. 1.9e-45;
86; Conservative 15; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER 1 1
SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
1810060009RIK PROTEIN.
IGH-1 OR 1810060009RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-PANCREAS;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98383416; PubMed=9717671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                     Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                 NCBI_TaxID=9796;
                                                                                                                              (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9D8L4
Q9D8L4;
                                                                                                                                                                                                                                                                                                                                                 Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09D8L4
셤
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Gaps

2 PELLGGPSVFLFPPKPRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61

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Gaps

ö

Indels

19;

Length 468;

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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IRR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00409; iG; 2.
SMART; SM00407; iGc1; 3.
SMART; SM00406; iGv; 1.
SMART; SM00406; iGv; 1.
SMART; SM00406; iG_MC; UNKNOWN_1.
SMART; PR002290; IG_MC; UNKNOWN_1.
                                                                                                                                                                                                                                   69.5%; Score 407; DB 11;
68.2%; Pred. No. 7.8e-37;
iive 16; Mismatches 19;
InterPro; IPR003600; Ig_like
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75; Conservative
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       099L25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  099125
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Q91Z05
ID Q9:
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Q99L25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 61
                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 463;
                                                       62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                             282 REEQFNSTERSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810066009 GENE.
                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.2%; Score 411.5; DB 11;
ilarity 67.9%; Pred. No. 2.4e-37;
Conservative 19; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 AA
                                                                                                                                                                                            463 AA
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                            099LC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99L31
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                                                                                                                                                     RESULT
Q99LC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 THREDINSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Indels
                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INCELLY, PPO0047; 19; 4.
SMART; SM00409; IG; 2.
SMART; SM00406; IGcl; 3.
SMART; SM00410; IGcl; 3.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 407; DB 11;
; Pred. No. 7.9e-37;
16; Mismatches 19;
473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473
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                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.C.
InterPro; IPR003600; Ig.Ilke.
InterPro; IPR0034006; Ig.MHC.
InterPro; IPR003596; Ig.MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.5%;
68.2%;
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                   Q9BQB8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BU10
                                                                                                             Q9BQB8
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                                         RESULT
                                                                           29BQB8
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                                                                                                                                               ACCOOR NAME OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || || : ::::::||:| |:: | :| | :| | 146 VFAIPPS-FASIFLIKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNAT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69
                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 THEDYNSTIRVYSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.2%; Score 142; DB 4; Length 375; 28.7%; Pred. No. 1.5e-07; live 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004476; AAH04476.1; -.
HSSP; P01857; IFC1.
                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC010327; AAH10327.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 AA; 51946 MW; CF625F008932AF12 CRC64;
                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 41.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 KRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 68.9%; Score 404; DB 11; Local Similarity 66.4%; Pred. No. 1.7e-36; les 73; Conservative 17; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
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TISSUE-LYMPH, LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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Gaps
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                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-RHABDOMYOSARCOMA;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC0001803, AAH06180.1; -- EMBL; BC001872; AAH01872.1; --
                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNROVNN (PROFEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
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SMART; SM00409; 1G; 2.
SMART; SM00406; 1G; 1.
SMART; SM00406; 1Gv; 1.
SMART; SM00410; 1G_like; 1.
SMART; SM00410; 1G_like; 1.
SEQUENCE 597 AA; 65300 WW; 2DAFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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28.7%; Pred. No. 2.7e-07;
ive 26; Mismatches 44;
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597 AA.
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                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
PRT;
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InterPro; IPR003597; Ig.cl.
InterPro; IPR003609; Ig.like.
InterPro; IPR003069; Ig.like.
InterPro; IPR003596; Ig.wHC.
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Matches 29; Conservative
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TISSUE=LYMPH, LYMPHOMA;
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NCBI_TaxID=9606;
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Q96AA6
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Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                              Length 597;
       InterPro: IPR00360; Ig_like.
InterPro: IPR00360; Ig_like.
InterPro: IPR003506; Ig_like.
InterPro: IPR003596; Ig_v.
InterPro: IPR003596; Ig_v.
InterPro: IPR00405; Ig_v.
SMART; SM00406; Ig_v.
SMART; SM00406; Ig_v.
SMART; SM00410; IG_like; I.
SMART; SM00410; IG_like; I.
PROSITE: PS00290; IG_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 597 AA; 65274 MW; 2DAFABFB7E055851 CRC64;
                                                                                                                                                                                   44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:20337).
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28.7%; Pred. No. 2.7e-07;
Live 26; Mismatches 44;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Best Local Similarity 28.79
Matches 29; Conservative
                                                                                                                                                                      Best Local Similarity 28.7
Matches 29; Conservative
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InterP
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Q96EY0
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Q96BB9
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 67.8 KDA PROTEIN.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                    24.2%; Score 142; DB 4; Length 613; 28.7%; Pred. No. 2.8e-07; Live 26; Mismatches 44; Indels
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                     Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001); -. EMBL; BC0008951; AAH09851.1; -. SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614
SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-PRIMARY B-CELLS FROM TONSILS;
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SEQUENCE FROM N.A.
TISSUE-LYMPH, AND LYMPHOMA;
Strausberg R.;
                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.79
Matches 29; Conservative
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SEQUENCE FROM N.A.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC017356, AAH17356.1; - Hypothetical protein
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| CRC64;                                                | 24.28: Score 142. DR 4. Length 618. |
| 2696E0A6                                              | DB 4.                               |
| D4C7(                                                 | 142.                                |
| 96DB                                                  | S. C. C.                            |
| 3Q SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64; | 24.28:                              |
| 618 AA;                                               |                                     |
| EQUENCE                                               | Query Match                         |
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7 2; Gaps 10 VFLEPPKPRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 69 Querry Match Best Local Similarity 28%; Pred. No. 2.8e-07; Matches 29; Conservative 26; Mismatches 44; Indels ö

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Search completed: June 21, 2002, 08:59:31 Job time: 1630 sec

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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAA1980.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAA1981.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAA1990.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAA1991.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAA1990.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAA1997.DAT:*
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
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                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-674-857-4
586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
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|   | Description                  |             | Human immunoglobul | Undefined ORF2 enc | Human IqG1 Fcqamma | Immunoqlobulin G1 | Human immunoqlobul | Human IqG1 Fc reqi | Human immunoqlobul | IgG1 Fc protein us | Human IgG1 Fc prot | Human IqG1 Fc reqi | Human immunoglobul |
|---|------------------------------|-------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|   | ID                           |             | -                  | AAR41684           | AAY42621           | AAR87023          | AAR97264           | AAW02305           | AAW47354           | AAY23637           | AAW92411           | AAY99937           | AAY97182           |
|   | DB                           | :           | 13                 | 14                 | 20                 | 16                | 17                 | 17                 | 19                 | 20                 | 20                 | 21                 | 21                 |
|   | Length                       | 1 1 1 1 1 1 | 110                | 110                | 116                | 212               | 212                | 212                | 212                | 212                | 212                | 212                | 212                |
| æ | Query<br>e Match Length DB 1 | 111111      | 100.0              | 100.0              | 100.0              | 100.0             | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              |
|   | Score                        |             | 286                | 586                | 586                | 586               | 586                | 586                | 586                | 586                | 586                | 586                | 286                |
|   | Result<br>No.                |             | 1                  | 7                  | m                  | 4                 | S                  | 9                  | 7                  | 80                 | σ                  | 10                 | 11                 |

| region of | Fc region of human | Human immunoglobul<br>Native IdG Fo redi | Native IgG Fc regi | Human IgG Fc 1 all<br>Human IgG Fc 1 all | Human IgG1 non-A F | Human 1961 A allot<br>Sequence of human | Immunoglobulin G F | Human 1961 FC prot<br>Human 1961 FC chai | Human IgG1 Fc regi | Human 1961 ninge/r<br>Human IqGqammal hi | Human Immunoglobul | Human immunoglobui<br>Human immunoglobui | Human partial 1961 | Human IgGgammal hi | Human ımmunoglobin<br>Human Fc (IqG1) | Amino acid sequenc | Human 1961 Fc regi | FC-MMP inhibitor t | TWP-Fc protein sed | Fc-TNF-alpha inhib | TNF-alpha inhibito | Fc-IL-1 antagonist<br>IL-1 antagonist-Fc | MMP inhibitor-Fc f | Ş         |                    |            |           |           |                    |   | otype response;            |            |            |         |           |           |            |              |    |            | allotypic determinant -<br>rapy with decreased<br>nune responses        | 4           |  |
|-----------|--------------------|------------------------------------------|--------------------|------------------------------------------|--------------------|-----------------------------------------|--------------------|------------------------------------------|--------------------|------------------------------------------|--------------------|------------------------------------------|--------------------|--------------------|---------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------------------------------------|--------------------|-----------|--------------------|------------|-----------|-----------|--------------------|---|----------------------------|------------|------------|---------|-----------|-----------|------------|--------------|----|------------|-------------------------------------------------------------------------|-------------|--|
| AAR03809  | AAB62062           | AAY72750<br>AAB07474                     | AAB07475           | AAB67201<br>AAB67202                     | AAB76421           | AAB/6422<br>AAP70173                    | AAP82508           | AAK16955<br>AAY96529                     | AAB98953           | AAB28690                                 | AAY95579           | AAY70251<br>AAE02642                     | AAY72915           | AAB80897           | AAB49155<br>AAY06617                  | AAY01372           | AAM50246           | AAB17957           | AAB16958           | AAB17951           | AAB17952           | AAB17953<br>AAB17954                     | AAB17958           | ALIGNMENT |                    | 110 AA.    |           | •         | 12 region.         |   | ); anti-all                |            |            |         |           |           |            |              |    |            | s having modified allo<br>allotypes in therapy<br>ng undesirable immune | English.    |  |
|           |                    |                                          |                    | 2 22                                     |                    |                                         |                    |                                          |                    |                                          |                    |                                          |                    |                    |                                       |                    |                    |                    |                    |                    |                    |                                          |                    |           |                    | in;        |           | γ)        | 1 CH2              | , | 2, 17                      |            |            |         | 445.      | 245.      |            |              |    |            | ing<br>type<br>desi                                                     |             |  |
| 212       | 212                | 212                                      | 218                | 218                                      | 218                | 224                                     | 224                | 228<br>228                               | 228                | . 232                                    | 232                | 232                                      | 232                | 232                | 232                                   | 235                | 235                | 243                | 247                | 248                | 248                | 248<br>248                               | 250                |           |                    | ; Protein  |           | st entry  | lin IgGl           | 7 | Glm(1,                     |            |            |         | 2WO-GB004 | 91GB-0005 | LTD.       |              |    | 42.        | 9 50 ⋅-1                                                                | c; 57pp;    |  |
|           | 0                  | 00                                       | 0                  | 100.0                                    | 0.0                | 0.0                                     | 0.0                | 0.0                                      | 0.0                | 0.0                                      | 0.0                | 00                                       | 0.                 | 0.                 | 0.0                                   | 0.                 | 0.0                | 0.0                | 00                 | 0.                 | 0.0                | 0.0                                      | 0                  |           |                    | lard       |           | (firs     | opn                |   | .gG1                       |            |            |         | 92        | 91        |            |              |    | 49162/     | antibodies<br>matching<br>of causir                                     | ig 4        |  |
| 100       | 100                | 100                                      | 100                | 100                                      | 100                | 1001                                    | 100                | 100                                      | 100                | 1001                                     | 100                |                                          | 100                | 100                | 1001                                  | 100                | 100                | 200                | 10                 | 100                | 100                | 100                                      | 100                |           |                    | standard   |           |           | nogl               |   | βė; I<br>Ab.               | ens.       | -A.        | 92.     | 2;        | 1;        | LYNXVALE   |              |    | c          | antibodi<br>matchin<br>of caus                                          | (±1         |  |
| 200       | 286                | 586<br>586                               | 286                | 586<br>586                               | 586                | 286<br>586                              | 586                | 286<br>586                               | 586                | 286<br>586                               | 586                | 7 8 6<br>7 8 6                           | 586                | 586                | 286<br>586                            | 586                | 586                | 286                | 286                | 586                | 286                | 286<br>586                               | 586                |           | т                  | AAR27680 s | AAR27680; | -MAR-1993 | Human immunoglobul | ; | Isoallotype<br>humanised A | Homo sapie | WO9216562- | -OCT-19 | -MAR-1992 | -MAR-1991 | (LYNX-) LY | יפאי אייפן ט |    | WPI; 1992- | Humanised a<br>useful for<br>likelihood                                 | Disclosure; |  |
| 3 5       | 14                 | 15                                       | 17                 | 18                                       | 20                 | 22                                      | 23                 | 25                                       | 56                 | 78                                       | 29                 | 3 50                                     | 32                 | 33                 | 35                                    | 36                 | 37                 | 30                 | 2 4<br>2 0         | 41                 | 42                 | 443                                      | 45                 |           | RESULT<br>AAR27680 | A          | A.A       | 10        | Hu                 | • | Is                         | HO         | W          | 01      | 12        | 12        | 7          | - 2          | ל  | WP         | Hu<br>us<br>li                                                          | Di          |  |
|           |                    |                                          |                    |                                          |                    |                                         |                    |                                          |                    |                                          |                    |                                          |                    |                    |                                       |                    |                    |                    |                    |                    |                    |                                          |                    |           | AAR                | e ×        | Y S       | TO        | XX<br>DE           | × | X                          | SO         | NA         | € B \$  | PF        | X A       | X A        | XX           | ΖX | DR<br>X    | K L L L                                                                 | XX<br>PS    |  |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pAH4602. This vector contains open reading frames encoding the heavy chain variable region (VH) of the antibody 128.1, an ampicillin resistence gene and a histidine (histidinol) selection marker. Transcription of the VH gene is from the VH promoter of the murine 27.44 gene. The vector also includes a heavy chain immunoglobulin engancer and the human gammal constant region (CH). The VH region of 128.1 was isolated by polymerase chain reaction and cloned into plasmid pAH4274. This was achieved by digesting the plasmid and the product with Ecogy and NheI. The VH gene was inserted in-frame with the human
                     In humans, IgG1 may exist as either of two allotypes at site 1, 2 or 17. The inventor's propose eliminating these allotypes by amino acid changes to agree with the sequences of IgG2, IgG3 and IgG4. None of the allotype sites (1, 2 and 17) are located within the CH2 domain. New "isoallotypes" should be suitable for therapeutic use in all patients. See AAR27678-R27681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light; chain; variable; constant; region; anti-human; transferrin; receptor; antibody; brain; capillary; endothelial cell; conjugate; neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke; epilepsy; Parkinsons disease; Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody conjugates specific for transferrin receptor - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 586; DB 13;
100.0%; Pred. No. 5.2e-52;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 11K; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR41684 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Undefined ORF2 encoded by pAH4602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US10206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0800458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-196742/24.
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                         110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ43844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9310819-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-1993,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          riden PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
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                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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The invention provides immunoglobulin E (IgE) antagonists comprising one or more of the FeepsilonRI receptor-binding determinant sites of human lgE. The antagonists include IgE variants comprising an immunoglobulin template and binding determinant sequences (bds) CDbds, EFbds and the sequence shown in AAV42581. The CDbds (CD loop binding determinant sequence) are selected from the sequences shown in AAV42577 and the EFbds (EP loop binding determinant sequences shown in AAV42578-V42580. The variants are selected from sequences shown in AAV42578-V42580. The variants are useful in raising and screening anti-IgE antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment and prophylaxis of allergic
gammal CH region CH at the 3' end of the VH-J region by means of a Nhel site. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to tract or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for diagnostic methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IgE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                               1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                   Immunoglobulin B; IgB; antagonist; FcepsilonRI receptor; human; bds;
receptor-binding; binding determinant sequence; anti-IgE antibody;
                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                          Length 110;
                                                                                                                                                                                                                                                                                                                                                                          61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                          100.0%; Score 586; DB 14;
100.0%; Pred. No. 5.2e-52;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Column 61-62; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY42621 standard; protein; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0232539
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94US-0178583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IgG1 Fcgamma2 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-579941/49.
                                                                                                                                                                        110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-0CT-1999
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases
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AAY42621
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the human immunoglobulin G1 Fc region, and was used in creating a B2LF2-immunoglobulin Fc fusion protein (BZLF2/Fc).

B2LF2 is a Epstein-Barr virus (EBV) protein. To create B2LF2/Fc, this sequence, the leader sequence of mouse interleukin-7 (IL-7) (see AAR87021), a Flag octapeptide (see AAR87022) and a flaxible linker (see AAR87024) are joined to the extracellular domain (residues 34 to 223) of the B2LF2 sequence (see AAR87020). The B2LF2/Fc fusion protein containing this sequence is referred to in claim 4. B2LF2 proteins are members of the C-type lectin family. The C-type lectin domain is found in type II membrane proteins. The B2LF2 protein is capable of binding the beta chain of a major histocompatibility complex (MHC) class II antigen. Fusion proteins with an oligomerising zipper domain (OZD), instead of an immunoglobulin Fc region, can also be created. B2LF2
                                                                                                                                                                                                                                                                                                                        BZLF2; epstein-barr virus; BBV; C-type lectin; beta chain; MHC; antigen; major histocompatibility complex; immunoglobulin; cytotoxic T cell; autoimmune disease; myasthenia gravis; multiple sclerosis; allergy; systemic lupus erythematosus; organ transplant rejection; asthma; IL-7; tissue transplant rejection; therapy; cancer; viral disease; mouse;
                                                                                 Gaps
                                                                                                      1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating e.g. asthma, cancer
                                                                                                                 ;
                                                          Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epstein-Barr virus BZLF2 fusion proteins - used for treating auto-immune disease, transplant rejection, allergy, asthma, cor viral infection.
                                                                                                                                                 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                             Farrah
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comeau MR,
                                                        Score 586; DB 20;
Pred. No. 5.6e-52;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 38-39; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen JI,
MK;
                                                                                                                                                                                                                                 ¥
                                                                                                                                                                                                                                AAR87023 standard; protein; 212
                                                        100.0%; Silarity 100.0%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMY ) IMMUNEX CORP.
(UMOR ) UNIY MISSOURI.
(USSH ) US NAT INST OF HEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US05348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0235397.
                                                                                                                                                                                                                                                                                                     Immunoglobulin G1 Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spriggs
                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВЭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Armitage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-393086/50
                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hutt-fletcher LM,
                        116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9530015-A2.
                                                        Query Match
Best Local Simil
Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                Inteleukin-7
                                                                                                                                                                                                                                                                            11-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alderson M,
                        Sequence
                                                                                                                                                                                                                                                      AAR87023;
diseases
                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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proteins inhibit antigen-specific antibody formation, proliferation of blood monounclear cells and cytotoxic T cell responses. They also exhibit superantigen-like activity. The proteins can be used for treating or preventing autoimmune diseases such as myasthenia gravis, multiple sclerosis and systemic lupus erythematosus. Also, for treating organ or tissue transplant rejection and for treating or preventing allergy or asthma. They can be used for treating cancer and viral disease, especially EBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins - useful for treating rejection, allergy, asthma, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HVS14; major histocompatibility complex; MHC; Class II; allergy, binding protein; inhibition; antigen presentation; superantigen; treatment; cancer; viral disease; immunoglobulin; IgG1; Fc region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 586; DB 16;
100.0%; Pred. No. 1.2e-51;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spriggs M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR97264 standard; protein; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunoglobulin G1 Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saimiri 14 programment services to the services of the service
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 32; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US15948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0485549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0351901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ď
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated Herpes virus autoimmune disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-287183/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9617939-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
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Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR97264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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AA.

212

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AAW47354 standard; protein;
                            AAW47354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY23637
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  AAW47354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The human IgG1 Fc region (AAW02305) can be used as a fusion partner for interleukin-17 receptor (IL-17R) proteins (see also AAW04184-85), allowing purification of recombinant IL-17R using protein A or protein G affinity chromatography. Fusions between Fc and HYS13 (see also AAW02387), a viral homologue of IL-17, and between Fc and murine CILA8 (AAW02386) were used to identify cells that express the murine IL-17R. Selected murine thymoma EL4 cells were used as a source of murine IL-17R CDNA (AAT33800).
                     Gaps
                                               Gaps
                                      1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktk 73
                                                                                                                                                                                                                                                                                                                                                                                                       encoding interleukin-17 receptor - useful for regulating immune inflammatory responses, or to suppress graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                    ;
  Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 212;
                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 586; DB 17;
100.0%; Pred. No. 1.2e-51;
iive 0; Mismatches 0;
100.0%; Score 586; DB 17; 100.0%; Pred. No. 1.2e-51;
                    ó
                    0; Mismatches
                                                                                                                                                                                                                     IgG1; interleukin-17 receptor; IL-17R.
                                                                                                                                            AAW02305 standard; Protein; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 33; 52pp; English.
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                                                                                                                                                                                                                                                                                                96WO-US04018
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Spriggs MK,
                    Conservative
                                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                    Fc region.
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-443184/44.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 AA;
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                 05-DEC-1996
                                                                                                                                                                                                                                                            WO9629408-A1
                                                                                                                                                                                                                                                                                                21-MAR-1996;
                                                                                                                                                                                                                                                                                                                   07-AUG-1995;
                                                                                                                                                                                                                                                                                                                             23-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                   Fanslow WC,
                                                                                                                                                                                                                                                                              26-SEP-1996.
                                                                                                                                                                                                    Human IgG1
                    110;
                                                                                                                                                               AAW02305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
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                                                                                                                                   AAW02305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complex class II beta chain, useful for treating, e.g. auto-immune diseases or transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence was used in the preparation of a synthetic construct containing the Epstein-barr virus (EBV) BZLF2 protein, which is capable of binding a beta-chain of a major histocompatibility complex (MHC) class II antigen. The protein can be used to inhibit antigen-specific antibody formation, peripheral blood mononclear cell proliferation and cytocoxic T-cell responses, e.g. in the prevention or treatment of autoimmune diseases, transplant rejection, allergies or asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                 BZLF2; beta-chain; major histocompatibility complex; MHC;
                                                                                                     class II; antigen; prevention; treatment; autoimmune disease; transplant rejection; allergy; asthma; super-antigen; IgG1; Epstein-barr virus; human; immunoglobulin G1; Fc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Farrah TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comeau MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 586; DB 19;
Pred. No. 1.2e-51;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Columns 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohen JI,
MK;
                                       Human immunoglobulin G1 Fc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
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                                                                                                                                                                                                                                                                                                                 95US-0430633.
                                                                                                                                                                                                                                                                                                                                                         95US-0430633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spriggs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Armitage RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and as a super-antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-192827/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hutt-Fletcher
                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                 28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                               28-APR-1994;
01-JUN-1998
                                                                                                                                                                                                                                  US5726286-A.
                                                                                                                                                                                                                                                                                                                                                           28-APR-1995;
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                                                                                                                                                                                                                                                                          10-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DXIXAX
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IgG1 Fc protein used to make BZLF2 fusion proteins.

RESULT

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-1996;
23-MAR-1995;
                                           21-MAR-1996;
                                                                        23-MAR-1995;
07-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6072037-A.
US5869286-A.
                     09-FEB-1999.
                                                               21-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY99937;
                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
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                                                                                                                                                                                                                                                                                                               The present sequence represents a protein used to create fusion proteins with the Bpstein-Barr virus BZLF2 proteins of the invention. The BZLF2 protein is capable of binding to a beta chain of a class II major histocompatibility complex antigen to inhibit an antigen-specific response. BZLF2 is useful for inhibiting antigen-specific antibody formation, the proliferation of blood mononuclear mononuclear cells, and cytotoxic T cell responses. BZLF2 is also useful for inhibiting undesirable antigen specific responses, e.g. in the treatment or prevention of asthma; for preventing or treating autoimmune disease; and for preventing tissue or organ transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IL-17R; human; interleukin-17 receptor; immunoregulator; inhibitor; T cell proliferation; T cell activation; organ; graft; rejection; autoimmune disease; allergy; asthma; treatment; inflammatory disease; B cell proliferation; immunoglobulin secretion; immunogen; IgGl; Fo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BZLF2 protein; beta chain; blood mononuclear mononuclear cell; Class II major histocompatibility complex antigen; proliferation; cytotoxic T cell response; antigen specific response; asthma; autoimmune disease; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 212;
                                                                                                                                                                                                                   Farrah TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 586; DB 20; Best Local Similarity 100.0%; Pred. No. 1.2e-51; Matches 110; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                   Comeau MR,
                                                                                                                                                                                                                האסבויסה M, Armitage RJ, Cohen JI,
Hutt-Fletcher LM, Spriggs MK;
                                                                                                                                                                                                                                                                                           Claim 2; Column 31-32; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                       Epstein-Barr virus BZLF2 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW92411 standard; Protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IgG1 Fc protein fragment.
                                                                                                                                                  95US-0430633.
94US-0235397.
97US-0936854.
                                                                                                                               97US-0936854
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                                                                                                                                                                                              (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                  WPI; 1999-418295/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                     212 AA;
                                                                                                                                                  28-APR-1995;
28-APR-1994;
24-SEP-1997;
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                                                               Homo sapiens
                                                                                                                               24-SEP-1997;
                                                                                   US5925734-A
                                                                                                         20-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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This sequence represents a human IgG1 Fc fragment which is used in the construction of a fusion protein with human interleukin-17 receptor [LI-178, LI-178 polypeptides have immunoregulatory activity. They can be used for inhibiting T cell proliferation, or for inhibiting T cell activation. In particular they can be used for preventing or treating organ or graft rejection, autoimmune disease, alleray or asthma. They can also be used for the prevention or treatment of inflammatory disease in proliferation or immunogalbulian secretion. The IL-17 polypeptides can also be used as immunogens, reagents in in vitro assays, or as binding agents for affinity purification procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                   Isolated interleukin-17 receptor DNA - used to develop products for treating e.g. organ or graft rejection, autoimmune disease, allergy, asthma or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 586; DB 20;
100.0%; Pred. No. 1.2e-51;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Column 31-32; 25pp; English.
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                                                         96US-0620694.
95US-0410535.
95US-0538765.
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95US-0410535.
96US-0620694
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Matches 110; Conservative
                                                                                                                                                                                                                                      Fanslow WC, Spriggs MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 1gG1 Fc region.
                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                               WPI; 1999-152766/13.
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A novel interleukin-17 receptor (IL-17R) was identified by screening a CDNA library from T cell thymoma EL4 cells, which were identified as binding fusion proteins comprising human immunoslobulin GI (19G1) Fc region and soluble IL-17 (CTA-8) protein or a homologous Herpesvirus saimiri (HSV) protein, designated HSV13. Suppressing rejection of a grafted syngeneic or allogeneic organ or tissue in a graftecioient involves transfecting the organ or tissue to be transplanted with DNA encoding soluble IL-17R, so that expression of IL-17R by the engrafted organ or tissue results in suppression of rejection. Soluble IL-17R fragments comprise residues 1-320 of the murine IL-17R, residues 1-320 of the human IL-17R, and fragments of the extracellular domain that bind IL-17. The method is useful for regulating an immunoresponse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for suppressing rejection of grafted organs or tissues in the recipient and for treating or preventing diseases like allergy, asthma and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri; HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic; anti-asthmatic; immunoglobulin G1; Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktk 73
                                                                                                                               Suppressing rejection of a grafted syngeneic or allogeneic organ or tissue in a graft recipient for organ transplantation involves transfecting the organ or tissue with DNA encoding soluble interleukin-17R receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 586; DB 21;
100.0%; Pred. No. 1.2e-51;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                 Example 1; Column 31-32; 27pp; English.
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                                              Yao Z;
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95US-0410535.
95US-0538765.
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Best Local Similarity 100.0
Matches 110; Conservative
                                              Spriggs MK,
  (IMMV ) IMMUNEX CORP.
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                                                                                          WPI; 2000-523862/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA;
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07-AUG-1995;
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                                              Fanslow WC,
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                                                                                                                                                                                                                                                                                                                                The present invention relates to a novel receptor that binds Interleukin (II-17, also known as CTLA-8) and a Herpesvirus saimiri homolog, HVS13. The receptor is a type I transmembrane protein which is referred to as IL-17R. Murine thymona EL4 cells were found to express a receptor for IL-17. An EL4 mammalian expression library was screened and cDNA encoding the receptor was identified (see AAA61238). The CDNA was used to isolate DNA encoding human IL-17R by cross species hybridisation. The human IL-17R cDNA and protein are described in that may be used with IL-17R cDNA and protein. Soluble forms of the receptor may be used to regulate immune responses, for example to suppress rejection of organ grafts. Antibodies to IL-17R consisting of amino acids 1-322 of murine IL-17R or research assays. Such antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-17R; interleukin-17 receptor; soluble; CTLA-8; Herpesvirus saimiri; HSV13; graft rejection; suppressor; immunosuppressive; anti-allergic; anti-asthmatic; immunoglobulin G1; Fc region.
                                                                                                                                                                         Antibodies immunoreactive with interleukin-17 receptor protein useful in interfering with receptor binding to CTLA-8, as components of diagnostic or research assays or in affinity purification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        may also be used in affinity purification of the receptor
                                                                                                                                                                                                                                                                                      Disclosure; Column 31-32; 25pp; English.
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                                                                                          Ζ;
                                                                                        Yao
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95US-0410535.
95US-0538765.
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  95US-0538765
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                                                                                          Fanslow WC, Spriggs MK,
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                                              (IMMV ) IMMUNEX CORP.
                                                                                                                                  WPI; 2000-411206/35.
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07-AUG-1995;
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07-AUG-1995;
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RESULT 11 AAY97182

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Example 1; Column 31-32; 26pp; English.
allergy or asthma in human
                                        invention relates to
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07-AUG-1995;
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 disease,
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                                                                                               A novel interleukin-17 receptor (IL-17R) was identified by screening a binding fusion proteins comprising human immunoglobulin GI (19G1) Fc region and soluble IL-17 (CTLA-8) protein or a homologous Herpesvirus saimiri (HSV) protein, designated HSV13. Regulating an Harmone or inflammatory response in a mammal comprises administering soluble IL-17R. Soluble IL-17R fragments comprise residues 1-320 of the mum IL-17R, and fragments of the mum IL-17R, and fragments of the an immunoresponse, for treating or preventing diseases like allergy, asthma and autofimmune diseases, and for suppressing rejection of grafted organs or tissues in the recipient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-17 receptor; IL-17R; CTLAB; antiinflammatory; antiallergic; immunosuppressive; organ rejection; graft rejection; autoimmune disease; allergy; asthma; IgG1; immunoglobulin G1; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-17 receptor protein useful for regulating immune functions and for preventing or treating organ or graft rejection, autoimmune
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                                                                                                                                                                                                                                                                                                                  Regulating, treating or preventing immune or inflammatory response mammal, especially organ or graft rejection, allergy or asthma, comprises administering interleukin-17 receptors
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                                                                                                                                                                                                                                                              100.0%; Score 586; DB 21; Length 212; 100.0%; Pred. No. 1.2e-51; Live 0; Mismatches 0; Indels 0
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Best Local Similarity 100.
Matches 110; Conservative
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Spriggs MK,
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                   WPI; 2000-548298/50
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                                                                                                                                                                                                                                 212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fanslow WC,
Fanslow WC,
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                                                                                                                                                                                                                                  Sequence
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Tries Invention Frailes to an institute and putting interpervising standard to an institution (CTLAR) and a herpesvirus standing (TTLAR) as soluble [L-17 protein (CTLAR) and a herpesvirus standing protein comprising an immunoglobulin For region, and used to screen for the expression of the IL-17R. The screening identified the novel receptor of the invention. IL-17R is a type I transmembrane protein that exhibits antiinflammatory, immunosuppressive, antiasthmatic and antiallergic activities, and is an inhibitor of T cell proliferation and activation. IL-17R can be used to regulate immune functions, and is useful for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. The present sequence represents the Fc region of human immunoglobulin G1 (1961). This fragment of IgG1 forms part of the IL-17 fusion protein used to identify IL-17R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention is directed towards assays for detection of interleukin-17 (IL-17), IL-17 receptor (IL-17R), and (antagonists or mimetics of) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTLA-8; interleukin-17; IL-17; IL-17 receptor; IL-17R; human; IgG1; immunosuppressive; antiallergic; antiasthmatic; antiinflammatory.
purified interleukin-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.04; Score 586; DB 21; Length 212; Best Local Similarity 100.04; Pred. No. 1.2e-51; Matches 110; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Columns 31-32; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fc region of human immunoglobulin IgG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB62062 standard; Protein; 212 AA.
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95US-0410535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to Interleukin-17 receptors (IL-17R), Interleukin-17 and their corresponding nucleic acid molecules. IL-17R is a Type I transmembrane protein which is used for regulating the immune response. The invention is useful for suppressing rejection of a grafted organ or tissue in a graft recipient. Soluble IL-17 (CTLA-8) receptors are useful for preventing or treating organ or graft rejection,
interaction between IL-17 and IL-17R. The assay kit comprises an IL-17R
              protein and a detecting reagent. The method is useful for inhibiting binding of IL-17 to cells expressing IL-17R. IL-17 receptors are also useful for preventing or treating organ or graft rejection, autoimmune diseases, allergy, asthma and inflammatory diseases in which activated T-cells play an important role. The present sequence represents FC region of human immunoglobulin IgG1, used for constructing a murine
                                                                                                                                                                                                                                                                                 1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                 14 apellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktk 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suppressing rejection of grafted organ or tissue in graft recipient, involves administering to recipient a composition comprising interleukin 17 receptor protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the Fc region of human immunoglobulin \lg G1 which is used for constructing fusion protein with Interleukin-17 receptor (IL-17R).
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                                                                                                                                                                                                               Length 212;
                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
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                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 110; Conservative
                                                                                                                   CTLA-8/Fc fusion protein
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                                                                                                                                                          212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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autoimmune disease, allergy, asthma, and inflammatory disease in which activated T-cells play a role. Soluble IL-17 fusion proteins are used to screen cells for the expression of IL-17 receptor. Derivatives of IL-17R are also used as immunogens, reagents in in vitro assays, or as binding agents for affinity purification procedures.
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                                                                                                                                                     Length 212;
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                                                                                                                                              100.0%; Score 586; DB 22;
100.0%; Pred. No. 1.2e-51;
tive 0; Mismatches 0;
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1 APPVAGPSVFLFPPKPKDTL.......CKVSNKGLPAPIEKTISKT
GenCore version 4.5
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Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pr and is derived by analysis of the total score distribution.

19 gamma - 2
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| 45                 |
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| e a printed, lon                                                                                                               | RESULT 1 G2HU IG2HU IG3HU IG gamma-2 C;Species: C;Date: 30. C;Accession R;Ellison, Proc. Artile: Li A;Title: Li A;Title: Li A;Molecule | RESULT 1  G2HU  Ig gamma-2 chain C regic (5, Species: Homo sapies C; Accession: A93906, A9; RFELLISON, J.; Hood, L. A; Fillison, J.; Hood, L. A; Fillison, J.; Hood, L. A; Ritle: Linkage and seans and seasion and seasion appropriate proteins and seasions A90752 A; Mancession: A90752 A; Modelle type: proteins and seasions A90752 A; Mancession: A90752 A; Mancession: A90752 A; Mancession: A90752 | Chain C region  Homo sapiens  154 26.4 4  161 27.6 5 5  164 26.4 4  Homo sapiens  Homo sapiens  A93906; A9280  J.; Hood, L.  J.; Hood, L.  J. A93906  A93906  Type: DNA  1-326 EBLV00  Type: DNA  Type: DNA  Type: DNA  Type: DNA  Type: DNA  1-326 is probabl  12, 1048-1054  is number: A92809  myeloma protein  Type: Protein  Type: Protein  1-19, 'Q', 21-57  Type: DNA  Type: DNA  1-19, 'Q', 21-57  Type: DNA  Type: Protein   428 1<br>429 1<br>429 1<br>(mence, rev<br>1809; A907<br>1.S.A. 79,<br>1.S.A. 79,<br>100554; GB<br>1005; MUID:<br>1005; MUID:<br>1009; MUID:<br>1009 | uman<br>uman<br>uman<br>uman<br>uman<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan<br>upan | ### 170.5 29.2 4.28 1 EHHU                                                                                                                                                                                                                                                                                                                                                                                                                 | chain c<br>hain pre<br>chain C<br>l-2000<br>l: PID:g6066056<br>evolutionary, an<br>region domains of | |
|---|---|---|---|---|---|---|---|
| 2b chain 2a chain 2a chain 3 chain c 4 chain c I chain c chain pre chain C -1 chain - chain C -1 chain2 chain2b chain -3 chain | A, Note R, Hofm MOI MOI MOI A, Titil A, Refe A, Roce A, Molee A, Resi R, Hofm Submit                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | A; Note: this sequence has since bear, Hoffmann, T.; Parr, D.M.  Mol. Immunol. 16, 923-925, 1979  A; Title: A note on the amino acid: A; Reference number: A93132; MUID:88  A; Contents: 2.1e  A; A; Accession: A93132  A; Molecule type: protein  A; Residues: 238-275 < HOF>  Submitted to the Atlas, March 1980  A; Reference number: A94591                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Parr, D. 6, 923-9 on the ber: A93 3132 : protei -275 <ho a94<="" berr,="" parl,="" td=""><td>45. 197. 47. 1932; MI 132; MI March</td><td>ce be<br/>acid<br/>JID:8</td><td>A;Note: this sequence has since been revised R;Hdfmann, T.; Parr, D.M. Miltie. Inmunol. 16, 923-925, 1979 A;Aitle: A note on the amino acid sequence of residues 381-391 of humar A;Reference number: A93132; MUID:80114419 A;Contents: 2.18 A;Accession: A9312 A;Molecule type: protein A;Residues: 238-275 <hof> R;Hofmann, T.; Parr, D.M. R;Hofmann, T.; Parr, D.M. Submitted to the Atlas, March 1980 A;Reference number: A94591</hof></td><td>of human immunoglobuli</td></ho>        | 45. 197. 47. 1932; MI 132; MI March                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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Miltie. Inmunol. 16, 923-925, 1979 A;Aitle: A note on the amino acid sequence of residues 381-391 of humar A;Reference number: A93132; MUID:80114419 A;Contents: 2.18 A;Accession: A9312 A;Molecule type: protein A;Residues: 238-275 <hof> R;Hofmann, T.; Parr, D.M. R;Hofmann, T.; Parr, D.M. Submitted to the Atlas, March 1980 A;Reference number: A94591</hof> | of human immunoglobuli                                                                               |
| -3 chain C<br>-1 chain C<br>-1 chain C<br>al antibod<br>-2 chain C<br>-2 c chain C<br>-1 chain C                               | A;Cont. A;Note ned R;Mils Bioche A;Titil                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ents: anno<br>: the rev<br>tein, C.;<br>m. J. 121<br>m. J. 121<br>e. Disulp<br>rence num<br>ents: anno                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | otation;<br>ised seq<br>Frangio,<br>217-22<br>hide bri<br>ber: A90<br>otation;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | zie, ;<br>lence o<br>ne, B.<br>5, 197.<br>Iges o<br>253; Mt                                                                                                                                                                                                                                                                                                                                                                      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having 60-Ala and hed R;Milstein, C.; Frangione, B. Biochem. J. 121, 217-225, 1971 A;Milstein Disulphide bridges of the heavy chain of human immunoglobulin G2. A;Reference number: A90253; MID:72033500 A;Reference number: myeloma protein Sa, disulfide bonds                                         | and 264-268<br>60-Ala and in the amid<br>jlobulin G2.                                                |

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C;Accession: S31866
R;Filpula, D.
Rubilted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein interactions of cloned gene produc A;Reference number: S31866
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G. Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
A;Accession: A23511
                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-377 <HUC>
A; Residues: 1-377 <HUC>
A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics:
A; Gene: GDB:IGHG3
A; Cross-references: GDB:119339; OMIM:147120
A; Cross-references: BB:119339; OMIM:147120
A; Map position: 14q32.33-14q32.33
A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMM>
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#sequence_revision 17-Mar-1997 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G; Species: Pan troglodytes (chimpanzee)
C; Species: Pan troglodytes (chimpanzee)
C; Species: Pan troglodytes (chimpanzee)
C; Species: Dave-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C; Accession: PT0207
R; Ehrlich, P. H; Moustafa, Z. A; Oestberg, L.
MOI. Immunol. 28, 319-322, 1991
A; Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Reference number: PT0207; MUID:91287716
A; Molecule type: mRNA
A; Residues: 1-234 < EHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 QYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 540; DB 2; L
Pred. No. 4.8e-47;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.1%; Score 537; DB 2; L
llarity 88.6%; Pred. No. 5.5e-47;
Conservative 4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.6%; Score 540; 94.3%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 94.3
Matches 100; Conservative
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A.Note: Homo sapiens (man)
C.Date: 06-Jan-1995 #sequen
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Best Local Similarity
Matches 101; Conserv
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C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C:Complex: An immunoglobulin heterotetramer; immunoglobulin c region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-085/Domain: immunoglobulin homology xIMA>
F:210-85/Domain: immunoglobulin homology xIMA>
F:239-306/Domain: immunoglobulin homology xIMA>
F:210-83,140-200,246-304/Disulfide bonds: #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:276/Filaliding site: carbohydrate (Asn) (covalent) #status predicted
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C.Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fig gamma 3 chain C region (allotype G3m(b)) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999 C;Accession: A2311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.6%; Score 540; DB 2; Length 37 Best Local Similarity 94.3%; Pred. No. 4.8e-47; Matches 100; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 583; DB 1; Best Local Similarity 100.0%; Pred. No. 1.8e-51; Matches 109; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: A60764
R; Huck, S; Lefranc, G; Lefranc, M.P.
Rmunogenetics 30, 250-257, 1989
A; Title: A human immunoglobulin IGHG3 allele (Gmb0, A; Reference number: A60764; MUID:90007613
                                                                             G.
            R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin (
Rférence number: A93157; MUID:69064124
A;Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                                              A; Cross-references: GDB:119338; OMIM:147110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma-3 chain C region, form LAT - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-377 <HUC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A60764
A; Status: preliminary
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                                                                                                                                                                                                    A; Gene: GDB: IGHG2
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Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni
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Matches 100; Conserv
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C; Species: Homo saptens (man)

C; Species: Homo saptens

C; Saccession: A93433; S36661; S33887; B99563; A90564; B91668; A91723; A02146

R; Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.

A; Reference number: A93433; MUID: 82274238

A; Accession: A93433

A; Molecule type: DNA

A; Residues: 1-30 EBLL>

A; Cross references: EMBL: 217370

A; Note: Lius sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, A; Note: Lys-330 is removed after translation

R; Harris, L.J.

Submitted to the EMBL Data Library, October 1992

A; Accession: S36861

A; Accession: S36861

A; Accession: S36861

A; Accession: S36861

A; Molecule type: DNA

A; Residues: 2-330 Glake,
A; Accession: S3687

A; Accession: S3687

A; Accession: S3687

A; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of a A; Reference number: S33887; MUID:83001943

A; Reference number: S33887; MUID:83001943
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A; Residues: 136-154, Q', 156-165, Q', 167-176, Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A; Residues: 136-154, Q', 156-165, Q', 167-176, Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R; Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       35 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 94
                                                                            A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069 C;Keywords: immunoglobulin F;1-22/Region: Escherichia coli outer membrane protein A precursor F;23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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9
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                                                                                                                                                                                                                                              91.8%; Score 535; DB 4; L6
87.7%; Pred. No. 9.8e-47;
ive 5; Mismatches 3;
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.7
Matches 100; Conservative
A; Accession: S31866
A; Molecule type: mRNA
A; Residues: 1-255 <FIL>
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A. Molecule type: protein
A. Residues: 1-96, "R', 98-197, "D', 199-238, "E', 240, "M', 242-266, "D', 268-271, "D', 273-330 <
A. Note: this sequence das the Glm(3) and Glm(non-1) markers
A: Note: this sequence das the Glm(3) and Glm(non-1) markers
B. Gall, W.E.; Edelman, G.M.
A: Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul
A: Reference number: A90565; MUID: 71064027
A: Contents: annotation; disulfide bonds
B: Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
B: Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
B: Dreker, E.; Physiol. Chem. 357, 1515-1540, 1976
A: Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunog enbrande cleavage products, and the disulfide bridges.
A: Reference number: A01667; MUID: 77070267
A: Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A hap position: 14932.33-14932.33
A; Introns: 99/1; 114/1; 224/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMI)
                                                                                                                                  A; Molecule type: protein
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A; Note: this sequence has the Glm(17) and Glm(17) markers
R; Schmidt, W.E.; Jungy, H.D.; Palm, W.; Hischmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1
A; Reference number: A91723; MUID: 83289131
A; Accession: A91723
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C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #text_change 01-Dec-2000
C; Date: 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S6939; S72664
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Blochem. 29, 54-60, 1995
Bur. J. Blochem. 29, 54-60, 1995
A; Reference number: S69339; MuID:95262687
A; Reference number: S69339
A; Accession: S6933
A; Accession: S69339
A; Accession: S69339
A; Accession: S69339
A; Residues: 1-374 < KHA>
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F;243-310/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/A:204,256-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
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87.7%; Pred. No. 1.3e-46;
ive 5; Mismatches 3; Indels
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A;Cross-references: GDB:120085; OMIM:147100
A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: B91668
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A. Wolecule type: protein
A. Wolecule type: protein
A. Wolecule type: protein
A. Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A. Note: the sequence of residues 42-76 was taken from the CHI region. Residue 12
A. Note: the sequence of residues 42-76 was taken from the reference that follows
B. Michaelsen, T. E.; Frangione, B.; Franklin, E.C.
J. Blol. Chem. 252, 883-889, 1977
A. Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat
A; Tontents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein
A; Accession: A92219
A; Mulcoll
A; Molecule type: protein
A; Residues: 12-97 < MIC>
A; Michaelsen: 12-97 < M
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A; Molecule type: protein
A; Note: this protein lacks most of the V region, all of the CHI region, and part of the A; Note: this protein lacks most of the V region, all of the CHI region, and part of the A; Note: Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deleti A; Reference number: A93915; MUD:82247835
A; Contents: heavy chain disease protein Omm
A; Accession: A93915.
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Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A; Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the Reference number: A90198; MUID:77021516
A; Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu
                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92191; A90198; A93915; A02149
C;Accession: A90442; A92219; A90198; Prelli, F.; Franklin, E.C.
BicFrangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Bichemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea
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A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156
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A;Note: this sequence may represent an allelic form or another gamma chain subclass
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A;Map position: 14932.33-14932.33
A;Map position: 14932.33-14932.33
A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid
E;203-270/Domain: immunoglobulin homology <IMM>
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64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                       C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 527; DB 1; I
Pred. No. 7.3e-46;
6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                           Iq gamma-3 heavy chain disease proteins - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A90442; MUID:81021548
A; Contents: heavy chain disease protein Wis
A; Accession: A90442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.48;
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Best Local Similarity 91.5:
Matches 97; Conservative
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A; Introns: 99/1; 111/1; 221/1
A; Introns: 99/1; 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region: immunoglobulin homology
C; Superfamily: immunoglobulin c region: immunoglobulin homology < IMI>
F; 30-85; Domain: immunoglobulin homology < IMI>
F; 30-10; Region: hinge
F; 30-10; Region: hinge
F; 30-10; Region: hinge
F; 30-10; Region: immunoglobulin homology < IMI>
F; 30-10; Region: immunoglobulin homology < IMI
F; 30-10; Region: immunoglobulin homology < IM
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A; Residues: 1-37 <ELL-
A; Note: the sequence was determined from the germline gene
R; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant
A; Reference number: A90249; MUID:70207560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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C;Species: Whom sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 PPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PP-----VAGPSVFLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNRALPAPIEKTISKAK 267
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DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4
A;Reference number: A90933; MUID:83157104
                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Pred. No. 1.5e-46;
5; Mismatches 3;
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Pred. No. 6.7e-46;
4; Mismatches 4;
          A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: $72664
A;Accession: $72664
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A;Cross-references: GDB:119340; OMIM:147130
                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
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A; Residues: 1-30;81-326 <PIN>
C; Genetics:
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Best Local Si
Matches 98;
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Best Local Si
Matches 100
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gramma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: 147162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
A;Title: Five putative subclasses of swine igG identified from the cDNA sequences of A;Reference number: 147158; MUID:95015845
A;Reference number: 147158; MUID:95015845
A;Accession: 147162
A;Retais: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Retaidues: 1-277 < KAC>
A;Cross references: EMBL:U03782; NID:9433129; PIDN:AAA52220.1; PID:9433130
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 qamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: 147161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147161
A;Reference number: 147161
A;Retus: prediminary; translated from GB/EMBL/DDBJ
A;Retus: prediminary; translated from GB/EMBL/DDBJ
A;Residues: 1-328 cKAC>
A;Cross_references: EMBL:U03781; NID:9433127; PIDN:AAA52219.1; PID:9433128
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147158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 277;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
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; Pred. No. 2.1e-39;
12; Mismatches 9
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79.8%;
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                                              Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Cecession: 147160
R;Kacskovic: 147160
R;Kacskovic: 147161
J: Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Accession: 147160
A;Accession: 147160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 147160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C rocal-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         If gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: I4/159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a S,Reference number: I4/158; MUID:95015845
A;Accession: I4/159
A;Reference number: I4/158; MUID:95015845
A;Recession: I4/159
A;Residues: I-328 «KAC>
A;Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
C;Genetics:
A;Gene: IgG3a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF 65
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80.8%; Pred. No. 8.1e-40;
iive 12; Mismatches 8; Indels
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80.8%; Pred. No. 8.1e-40;
Live 12; Mismatches 8; Indels
138 QFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 NSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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Best Local Similarity 80.89
Matches 84; Conservative
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Best Local Similarity
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RESULT 11

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δ 엄 δ g RESULT

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Search completed: June 21, 2002, 08:37:54
Job time: 428 sec
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N.Alternate names: Ig gamma-1 chain C region (clone 8.10)

S.Species: Bos primigenius taurus (cattle)

C.Species: Bos primigenius taurus (cattle)

C.Accession: $22080; $06610; A31303

R.Sanders, P.G.

R.Sand
                                                                                                         a
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the CDNA sequences of A:Title: Five putative subclasses of swine IgG identified from the CDNA sequences of A:Tkeference number: I47158; MUID:95015845
A:Reference number: I47158
A:Reference references: I47158
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: I-328 KARC>
A:Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
A:Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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A.Introns: 98/1; 111/1; 221/1
C.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:161-225/Domain: carbohydrate (Asn) (covalent) *status predicted
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A; Residues: 142-470 <SYM>
A; Cross-references: EMBL:X16701
A; Note: the sequence was determined from the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.5%; Score 452; DB 2; 79.8%; Pred. No. 3.4e-38;
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Best Local Similarity 79.8 Matches 83; Conservative
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CD4-gamma 2 chimeri
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3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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Human CD4-gamma2 c
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                                                                                                                                                                                                                                                         1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPSSIEKTISKTK 109
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                  747574 seqs, 111073796 residues
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Listing first 45 summaries
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AAB67203
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AAY06895
AAY06895
AAR466782
AAR46678
AAR85079
AAB80883
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AAY54997
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Maximum DB seq length: 200000000
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| CD4-gamma2 chimeri Humanised 323/A3 ( Human 1gG2 chain of The heavy chain of CD4-IgG2 chimeric Human CD4-IgG2 chimeric Human IgG2 chimeric Human IgG2 chimeric Human IgG2 chimeric Human IgG2 chimeric Hanan IgG2 chimeric Hanan IgG2 chimeric Hanan IgG2 chimeric Heavy chain of ful Human IgG2 chimeric A33 Chimeric recep Z33 GG21Az chimer Mutated.CH2 sequen Heavy chain consta | c)<br>c)<br>c)<br>seq<br>gra<br>nal<br>nal                                                       |
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| AAB67322<br>AAB72230<br>AAX931670<br>AAX931670<br>AAX931670<br>AAX93701<br>AAX93701<br>AAX93701<br>AAX93703<br>AAX93703<br>AAX93703<br>AAX93703<br>AAX93703<br>AAX93704<br>AAB667323<br>AAX946679<br>AAR30775<br>AAR30775<br>AAR30775<br>AAR30775<br>AAR30786<br>AAR30786<br>AAR30786<br>AAR30786<br>AAR30786<br>AAR30786<br>AAR30786<br>AAR30786<br>AAR30786<br>AAR30786<br>AAR30786<br>AAR3060                                                                                                                                                                                                                                            | 74299474<br>743394474                                                                            |
| 25000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 7<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1 |
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## ALIGNMENTS

RESULT

Polymerase chain reaction; primer; PCR; amplify; murine; pAH4625; heavy; light; chain; variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell. Undefined ORF2 encoded by plasmid pAH4625. AAR41709 standard; Protein; 109 AA. 92WO-US10206. 91US-0800458 20-OCT-1993 (first entry) WPI; 1993-196742/24. N-PSDB; AAQ43846. (ALKE-) ALKERMES INC 24-NOV-1992; 26-NOV-1991; WO9310819-A. 10-JUN-1993. Synthetic. Friden PM; AAR41709; AAR41709 

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The sequences given in AAR41707-09 are encoded by the expression vector pAH4655. This vector represents the cloning of the human gamma isotype, gamma-2, with the variable region of the murine monoclonal antibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CHI, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, also be used for diagnostic methods.
Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                     Disclosure; Fig 17J; 151pp; English.
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109 AA; Sequence

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                                 0; Gaps
                                                                        1 APPVAGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
98.6%; Score 572; DB 14; Length 109; 98.2%; Pred. No. 1e-51; ive 1; Mismatches 1; Indels
                                                                                                                                    61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                               1; Indels
                            Matches 107; Conservative
               Similarity
 Query Match
                  Local
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AAY54997 standard; protein; 109 AA.
                    Mutated CH2 sequence G2deltaa.
              (first entry)
              17-FEB-2000
        AAY54997;
AAY54997
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Binding molecule; CH2 sequence; complement dependent lysis; FcgammaRIIb; cell-mediated destruction; human: immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocytosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune disorder; autoimmune haemolytic anaemia; inflammatory disease; autoimmune thrombocytopaenia; arthritis; erythroblastosis foetalis; neonatal alloimmune thrombocytopaenia, Goodpastures disease; therapy; sickle cell anaemia; coronary artery occlusion. W09958572-A1 Synthetic.

(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD. Williamson LM; 99WO-GB01441 98GB-0009951 Armour KL, Clark MR, 07-MAY-1999; 38-MAY-1998;

WPI; 2000-039075/03

99US-0116023.

(GETH ) GENENTECH INC.

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binding molecule of the invention. The recombinate binding molecule of the invention. The recombinate binding molecule of the invention. The recombinate binding molecule of binding a target molecule without triggering complement comprises: (a) a binding domain capable of binding a target molecule; and dependent lysis, or the cell-indidated binding a target molecule; and comparises: (a) a binding domain capable of binding a target molecule (especially FegammaRID completion of a human immunoglobulin G (IgG) heavy chain. The binding mannequolulin G (IgG) heavy chain. The binding molecule can be used to prevent or inhibit the binding of a second binding molecule, e.g. an antibody, to the target molecule. The binding molecule is useful for the treatment of graft-vs-host disease, organ transplant rejection, bone-marrow transplant rejection, autoimmunity (e.g. vasculitis, autoimmunity molecule is vasculitis, autoimmunity can around and architis), alloimmunity ceg. foetal/neonatal alloimmune thrombocytopaenia, asthma and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN chrobiastosis foetalis), Goodpastures, sickle cell anaemia and coronary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FegammaR and desirable con-tuman amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent con-tumen amino acids, and are therefore likely to have reduced immunogenicity. Further, they still bind Protein A, which is consistent con-tument and allowed thromboty.
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                     Immunoglobulin-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties -
                                                                                                                                                         sequence represents the mutated CH2 molecule G2deltaa, and is a
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98.6%; Score 572; DB 21; Length 109;
Best Local Similarity 99.1%; Pred. No. 1e-51;
Matches 108; Conservative 0; Mismatches 1; Indels (
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                                                                                                          Claim 12; Fig 17; 81pp; English.
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produce Fc region-containing by the state of the section of the produce Fc region-containing by the section of the section of the variant polypeptides that have altered effector. The fc region of the variant polypeptides that have acid modifications in the Fc region. The variant polypeptides are useful for treating and LFA-1-mediated disorders. Where the polypeptide binds the HER2 and LFA-1-mediated disorders. Where the polypeptide binds the HER2 creeptor, the disorder preferably is HER2-expression of the HER2 center. Such cancers include breast cancer, squamous cell cancer, small-cell lung cancer, normal cell lung cancer, plioblastoma, cervical cancer, varian cancer, bladder cancer, hepatoma, colon cancer, colorectal cancer, hepatoma, colon cancer, colorectal cancer, liver cancer, liver cancer, liver cancer, hepatoms, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer.
                                                                                New Fc region-containing polypeptides that have altered effector function due to one or more amino acid modifications in the Fc region, useful in the treatment of cancer and allergic conditions such as
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Pred. No. 2.4e-51;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB07474-78 represent native IgG Fc regions.
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Best Local Similarity 98.2%;
Matches 107; Conservative
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                                                 WPI; 2000-476035/41
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This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides represented in ABM56550 - AAB76420 and AAB76432 - AAB76509 are examples of the ErbB2 binding ligands of the invention. Sequences AAB76421 - AAB76431 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain
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                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a fusion protein, comprising a peptide ligand and an immunoglobulin (Tg) constant region multimerization domain (Ib). The hybrid molecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used. For example the peptide ligand can bind ErbB2. The peptide ligand may bind to and inhibit the activity associated with a particular
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                                                                                                                                                                                                                                                                                                         Length 217;
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Pred. No. 2.4e-51;
1; Mismatches 1; Indels
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                                                     Disclosure; Fig 2; 69pp; English.
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Best Local Similarity 98.2%;
Matches 107; Conservative
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                                                                                                                                                                                                                                                      217 AA;
                                                                                                                                                                                                                    target molecule.
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The present sequence is human immunoglobulin G2 (IgG2) constant region mature protein. 19G2 forms a fusion protein with human erythropoietin (EPO). EPO has improved biological activity and an extended serum half life greater than 20 hours. The present invention relates to modified EPO forms such as fusion proteins comprising a FC portion of an immunoglobulin (Ig) molecule and an EPO molecule (FC-EPO). The FC portion is fused covalently through its C-terminus directly or indirectly to the modified or mutated. The invention also relates to non-fused EPO molecules which have a pattern of cysteines or disulphide bonding which
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                     disorders characterized by over expression of HER2/Erbb2 such as cancers, diseases of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgery, strokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes.
ErbB2 with naturally occurring ligands, and may be used to treat
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Fc portion of an immunoglobulin molecule and a target molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            Score 572; DB 22;
Pred. No. 2.4e-51;
1; Mismatches 1;
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98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-367563/38.
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE02643;
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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is distinct from human or animal EPO. Pharmaceutical compositions containing EPO are useful in the treatment of EPO deficient diseases such as amaemia, renal failure, HIV infection, blood loss and chronic disease that can be treated with haematopoietic growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion protein; vaccine; cytokine; immunoglobulin; autoimmune disease; infectious disease; infilammatory disease; neoplastic disease; cancer; immunologic disease; immune response; malaria; tuberculosis; hepatitis; AIDS; influenza; interleukin; IL-2; Ig; human.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                        1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                         ;
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                                                                                                                          Length 326;
                                                                                                                                                                                                                                                                  61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                         Indels
                                                                                                                         Score 572; DB 22;
Pred. No. 3.9e-51;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "interleukin-2 (IL-2)"
154..381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Fig 10A-E; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                              AAY06895 standard; Protein; 381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human IL-2/Ig fusion protein.
                                                                                                                          98.6%;
ilarity 98.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vaccine compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-254931/21
                                                                                                                                          Best Local Similarity
Matches 107; Conser
                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX34598
                                                                               326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                           AAY06895;
                                                                                Sequence
                                                                                                                              Query Match
Best Local S
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08-AUG-1994
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                                                                                            Query Match
Best Local S
                                                               Sequence
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Region
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an provide for enhancement of one or more immunologic parameters such a antibody response, a cellular proliferative response as well as ytotoxic T-lymphocyte levels. In addition the Ig can increase the inculating half life of the cytokine. The present sequence represents human interleukin-2 (IL-2)/Ig fusion protein.
                                                                                                                                             Gaps
                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery; chimeric; increased serum half life; HIV infection; AIDS; ss.
                                                                                                                                   1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for treatment, prevention and diagnosis of HIV infection
                                                                                                               ;
0
                                                                                           Length 381;
                                                                                                                                                                          Indels
                                                                                         Score 572; DB 20;
Pred. No. 4.7e-51;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                             CD4-gamma2 chimeric heavy chain homodimer.
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                 AAR26782 standard; Protein; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 3; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              217..325
/label= CH2
326..433
/label= CH3
                                                                                          Query Match 98.6%;
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-US01143
                                                                                                                                                                                                                                                                                                                                                                                                      /label= CD4
217..325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0653684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROG-) PROGENICS PHARM INC
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maddon PJ;
                                                                                                                                                                                                                                                                                                                                                               chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-300034/36.
                                                              381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ28088
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-1992
                                                                                                                                                                                                                                                                                         06-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9213947-A
                                                              Sequence
                                                                                                                                                                                                                                                                     AAR26782
                                                                                                                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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CD4+ cells and block the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in a assay for HIV or SIV infection, and it can also be linked to toxins, eg Diphtheria, Pseudomonas exotoxin A (domains I or II) or the deglycosylated A-chain
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                           1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV; human immunodeficiency virus; radionuclide; toxin; therapy; treatment; imaging; detection; targetting.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-1gG2 immuno:conjugates - used to kill HIV-infected cells and to ima and stage HIV infection
                                                                                                                                                                                                                            Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                       Score 572; DB 13;
Pred. No. 5.5e-51;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205..216
/label= Hinge Region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CH2 Region.
326..432
/label= CH3 Region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD4-gamma 2 chimeric heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR46678 standard; Protein; 432
                                                                                                                                                                                                                         98.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93WO-US07422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                     Matches 107; Conservative
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N-PSDB; AAQ57750.
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                    AA;
                                                                                                                                                    432
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                                                                                                                                                                                                                                                                                                                                                                                                           CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging; prognosis; envelope glycoprotein burden; human.
                                                                                                                                                                                        Human CD4-gamma 2 chimeric heavy chain homodimer amino acid sequence.
                                                                                                                                                   Gaps
infected subjects to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate comprising the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject.
                                                                                                                                                                         1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to heterotetramer of CD4-immunoglobulin chimeras
                                                                                                                                                  ó;
                                                                                                                            Length 432;
                                                                                                                                                                                                                        Indels
                                                                                                                            Score 572; DB 15;
Pred. No. 5.5e-51;
                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                              AAY85079 standard; Protein; 432 AA
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93WO-US07422.
95US-0379516.
                                                                                                                            98.6%;
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                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                   Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maddon PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-269502/23.
                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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03-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                      AAY85079;
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                                                                                                                               Query Match
                                                                                                                                            Local
                                                                                                                                                                                                                                                                                        10
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surface of helper T lymphocytes, cells of the monocyte/macrophage lineage and dendritic cells. CD4 associates with major histocompatibility complex (MHC) class II molecules on the surface of antigen presenting cells to mediate efficient cellular immune response interactions. In humans CD4 is the target of interaction with the human immunodeficiency virus HIV. The immunoconjugate is used to kill cells infected with HIV, and for treating or preventing infection. It is also used for imaging HIV-infected tissues (for staging or prognosis of infection, and for assessing efficacy of treatments). The immunoconjugate is also used to determine the HIV envelope glycoprotein burden, once determined, this information is used in the staging and prognosis of HIV infected patients. The immunoconjugate should be active against all strains of HIV (since the immunoconjugate should be active against all strains of HIV (since the immunoconjugate should be active against all strains of HIV (since the immunoconjugate intracellularly and secreted efficiently from mammalian calls, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell, or treating a subject having CD4+ cells infected with HIV involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or treating a subject having CD4+ cells infected with HIV involves using CD4-1gG2 chimeric heterotetramer to form a complex with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 572; DB 21; Length 432; pred. No. 5.5e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4-IgG2 chimeric heterotetramer; amma 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human CD4-gamma2 chimeric heavy chain homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB80883 standard; Protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.6%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0485372.
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92US-0960440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Anti-HIV; CD4·
immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-264981/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF77829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6187748-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB80883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
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chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4: 1962 = immunoglobulin gamma 2). CD4 is a cell surface of ylycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors CD4-IGG2HC-PRCCW(VI) and CD4-LCC-PRCCW(V(2), respectively. The method is used to inhibit infection of a CD4-cell by a HIV and to prevent CD4-cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4-cells infected with HIV. The present sequence is human fusion protein: CD4-gamma2 chimeric heavy chain homodimer. This sequence was used in the method of the present invention. ö CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 Gaps 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60 radionuclide linked to heterotetramer Immunoconjugate for treating human immunodeficiency virus-infected ö subject, consists of cytotoxic radionuclide linked to heterotet comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappalight chains Length 432; Indels CD4-gamma2 chimeric heavy chain homodimer protien. Score 572; DB 22; Pred. No. 5.5e-51; 1; Mismatches 1; Immunoconjugate; chelator; chimeric; HIV; AAB67322 standard; Protein; 432 AA 98.6%; 98.2%; 95US-0477460. 92US-0927931. 93US-0379516. human immunodeficiency virus 99US-0329916 93WO-US07422 (PROG-) PROGENICS PHARM INC. (first entry) Query Match
Best Local Similarity 98.2'
Matches 107; Conservative Maddon PJ, Allaway GP; WPI; 2001-158582/16. 432 AA; Homo sapiens US6177549-B1 10-JUN-1999; 23-APR-2001 23-JAN-2001 07-JUN-1995; 07-AUG-1992 06-AUG-1993; Sequence AAB67322; \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ õ 셤 ç g

The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterotetramer having two chimeric CD4-1gG2 heavy chains encoded by an expression vector CD4-1gG2HC-pRcCMV and two chimeric CD4-kappa light chains encoded by an expression vector

Disclosure; Fig 3; 43pp; English.

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This invention relates to a combination of an anti-Ep-CAM (cyclic adenosine monophosphate) antibody with a chemotherapeutic agent, that is capable of arresting Ep-CAM antigen expressing cells in the synthesis (S) phase or the second growth phase (M) of cell enlargement (G2)/DNA replication. The antibody exhibits cytostatic activity and is useful in the manufacture of a medicament for use in anti-cancer therapy, characterised in that a chemotherapeutic agent, which is capable of arresting Ep-CAM antigen expressing cells in S or in G2/M, is arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-administered to a patient with an anti-Ep-CAM antibody. The combination is useful for treating cancer, particularly colorectal cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell ung acancer. The present sequence represents the heavy chain of anti-Ep-CAM antibody known as humanised 323/A3 (IgG2cys) which can be used in the combination of the invention.
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Combination for treating cancer (e.g. breast, gastric or prostate cancers), or in the manufacture of a medicament for anti-cancer therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody with a chemotherapeutic agent -
                                                                                                                                                                                                                   Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis; chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
                                                                                                                                                                Gaps
                                                                                                                                                                                               1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised 323/A3 (IgG2cys) antibody heavy chain amino acid sequence.
CD4-kLC-pRcMV. The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, for the treatment and prevention of infection with HIV.
                                                                                                                                                                ö
                                                                                                                            Length 432;
                                                                                                                                                                                                                                                                                    61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                Indels
                                                                                                                                                                1;
                                                                                                                            Score 572; DB 22;
Pred. No. 5.5e-51;
                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thurmond LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 18; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         AAB72230 standard; Protein; 442 AA
                                                                                                                          98.6%;
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knick VC, Stimmel JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-182729/18;
N-PSDB; AAF63376.
                                                                                                                          Query Match
Best Local Similarity
                                                                          432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy chain.
                                                                                                                                                           Matches 107;
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555555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isotype 2 (1962, C-gamma-2). C-gamma-1 (see AAY31669) and C-gamma-3 (see AAY31671) bind For Ecceptors with high affinity, whereas C-gamma-4 (see AAY31671) has 10-fold lower binding affinity and C-gamma-2 does not bind to For Ecceptor gamma. The invention provides methods for the genetic construction and expression of antibody-based fusion proteins with enhanced circulating half-lives. The fusion proteins lack the ability to bind to immunoglobulin FC receptors, either as a consequence of the antibody isotype used for protein construction, i.e. a C-gamma-2 constant region (FC) or c-gamma-4 Fc receptor, or through directed mutagenesis of antibody isotypes that normally bind Fc receptors, i.e. C-gamma-1.

or C-gamma-3. The methods can be used for to increase the correction such as a non-immunoglobulin (Ig) protein such as circhiating half-life of a non-immunoglobulin (Ig) protein such as a lymphotoxin or a colony stimulating factor, a
                                                            ö
                                                                                            Gaps
                                                                                1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody-based fusion proteins, used for the delivery of e.g. cytokine, ligand-binding protein or protein toxin to target cells
                                                                                                                                                                                                                                                                                1962; C-gamma-2; antibody; fusion protein; circulating half-life; human; drug delivery.
                                                            ö
                                                                                                                                                                                                                                                                                                                                                           /note= "the identity of these residues is not
    specified"
                                      Length 442;
                                                                                                                                       61 REEQFINSTERVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                            1; Indels
                                       Score 572; DB 22;
Pred. No. 5.7e-51;
L; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wesolowski J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 32-33; 41pp; English
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                    AAY31670 standard; Protein; 443 AA
                                                              1;
                                          98.6%;
98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LEXI-) LEXIGEN PHARM CORP.
                                                                                                                                                                                                                                              (first entry)
                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lan Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-527594/44.
                                                                                                                                                                                                                                                                 Human IgG2 chain C.
                                                     Similarity
             442 AA;
                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            W09943713-A1
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                                                                                                                                                                                                                                              09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gillies SD,
                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1999
                                                      Best Local Sin
Matches 107;
                                                                                                                                                                                                                         AAY31670;
              Sequence
                                           Query Match
                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                           AAY31670
                                                                                                                                                                                 RESULT
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Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytotoxic T-lymphocyte antigen
and light chain sequences, useful
                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a heavy chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)-4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1. CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disperses, disbetes and graft rejection) and proliferative disorders dispease, diabetes and up-regulate immune system to up-regulate immune system to up-regulate immunodeficient disorders.
                                                                                                                                                                                                                                                                                                                                                      1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davis CG;
ligand-binding protein, e.g. CD4, CTLA-4, TNF receptor or an interleukin receptor, or a protein toxin (claimed). The fusion proteins are used to deliver selectively the second non-Ig protein to a target cell in vivo so that the second non-Ig protein exert a localised biological effect.
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                  Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPSSIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanke JH, Gilman SC,
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                               Score 572; DB 20;
Pred. No. 5.7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The heavy chain of immunoglobulin clone 11.2.1.
                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel antibodies capable of binding (CTLA)-4 containing specified heavy for treating, e.g. immune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 22q; 157pp; English.
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                                                                                                                                                                                                                                                  98.6%;
98.2%;
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                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                           443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA46898
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                                                                                                                                                                                                                                                                                                                 107;
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Best Local $
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                                                                                                                                                                                                                                                                                                                 Matches
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451 AA; Sequence So

0; Gaps Query Match

98.6%; Score 572; DB 21; Length 451;
Best Local Similarity 98.2%; Pred. No. 5.8e-51;
Matches 107; Conservative 1; Mismatches 1; Indels

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Search completed: June 21, 2002, 08:36:05 Job time: 319 sec

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A; Molecule type: DNA
A; Residues: 1-377 <HUC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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19 gamma chain C
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                  Compugen Ltd
                                                                                                                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                  283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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A23511
A23511
B31866
GHHU
GGHU
GGHU
147160
147160
147161
A7162
GGGP
C3054
C3054
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match
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                                                                                                        Run on:
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No.
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gamma-1 chain C
epsilon-chain -
epsilon chain C
heavy chain pre
epsilon chain C
       gamma-2b chain
gamma-2b chain
gamma-2c chain
gamma-2b chain
gamma-2c chain
gamma-2a chain
gamma-2a chain
gamma-2a chain
GGAMS11
SA0295
SO6611
SO1321
PSO0137
PSO019
B30503
A30503
A40732
S14236
I36948
EHHU
329
4474
4474
4476
3327
3328
3328
1112
1112
1123
428
428
428
410
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401
333
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323
313
310
210
264
110
264
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110
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115
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u) with an IGHG4 conv
C; Species: Homo sapiens (man)
C; Species: As (man)
C; Species: As (man)
C; Species: As (man)
C; Species: As (man)
C; Species: S
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C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin C; Keywords: immunoglobulin F; 20-85/Domain: immunoglobulin homology <IMM>
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Gaps ö Length 377; Indels 100.0%; Score 585; DB 2; ilarity 100.0%; Pred. No. 9.5e-52; Conservative 0; Mismatches 0; Best Local Similarity Matches 110; Conserv

1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60

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A:Cross-references: "GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056 C;Genetics:

A;Cross-references: GDB:119339; OMIM:147120 A;Map position: 14q32.33-14q32.33 A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3 C;Superfamily: immunoglobulin C region; immunoglobulin homology

86

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A; Wolecule type: DNA
A; Residues: 88-113;235-330 <TAK>
A; Residues: 88-113;235-330 <TAK>
A; Cross-references: EMBL:217370
B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma Biochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq A; Reference number: A90563; MUID:71064024
A; Contents: myeloma protein Eu
A; Accession: B90563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-330 < LLL>
A; Residues: 1-330 < LLL>
A; Cross-references: EMBL: 217370
A; Cross-references: EMBL: 217370
A; Note: Lys. 330 is removed after translation
A; Note: Lys. 330 is removed after translation
B; Harris, L.J.
B; Harris, L.J.
A; Reference number: S33904
A; Reference number: S33904
A; Accession: S36861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Molecule type: DNA
A; Residues: 2-330 <HBAD: 217370
A; Tesaklues: 2-350 <HBAD: 217370
B; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of A; Reference number: S33887; MUID:83001943
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A; Residues: 1-34, '0', 36-96, 'K', 98-115, '0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A; Residues: 1-34, '0', 36-96, 'K', 98-115, '0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A; Note: this sequence has the GIm(17) and GIm(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl
A; Recence number: A91723; MUID: 83289131
A; Contents: myeloma protein KOL; disulfide bonds
A; Accession: A91723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E' A; Note: this sequence has the Gim(non-1) markers, 239-Glu and 241-Met R; Ponstingl, H.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 A; Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A) Molecule type: protein A) Residues: 1-96, "K', 98-135 < CUN>
A) Residues: 1-96, "K', 98-135 < CUN>
A) Note: this sequence has the Glm(3) marker, 97-Arg
R) Ritishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochamistry 9, 317-3181, 1970
A; Title: The covalent structure of a human gammad-immunoglobulin. VIII. Amino acid
A; Réference number: A90564; MUID:71064025
                                                                                                                                                                                                                                                                                                                                                            C.Species: Homo sapiens (man)
C.Sacies: Homo sapiens (man)
C.Sacies: Jana-1981 #sequence revision 18-Aug-1982 #text_change 16-Jul-1999
C.Sacession: A94433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R.Ellison, J.W.: Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 40714479, 1982
A.Fitle: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A.Reference number: A93433; MUID:82274238
39 APELLGGPSVFLFPPRPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                 99 PREEQYNSTYRVVSVLIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148
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A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: B91668
                                                                                                                                                                                                                                                                                                                             gamma-1 chain C region - human
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C; Accession: S31866
C; Accession: S31866
A; Relaterate number: S31866
A; Reference number: S31866
A; Residues: 1255 cFILD
A; Cross-references: EMBL: X70421; NID: 933068; PIDN: CAA49866.1; PID: 933069
C; Keywords: immunoglobulin
F; 122/Region: Escherichia coli outer membrane protein A precursor
F; 23-255/Region: human Ig gamma-1 chain C region
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C; Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C; Accession: P70207
Mol. Immunol. 28, 319-322, 1991
A; Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Rithe: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Rithe: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Reference number: P70207
A; Residues: 1-234 < CHR>
A; Residues: 1-234 < CHR>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 48-117/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                   1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 84
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                                                                                                                                 Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                 61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
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Pred. No. 3.2e-50;
2; Mismatches 2;
                                                                                                                                 100.0%; Score 585; DB 2; 100.0%; Pred. No. 9.5e-52;
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                                                                                                                                                                                                  0; Mismatches
          C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMM>
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Best Lgcal Similarity 96.4%;
Matches 106; Conservative
                                                                                                                                                                                                     Matches 110; Conservative
                                                                                                                                 Query Match
Best Local Similarity
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Best Local Si
Matches 106;
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60

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5; Mismatches
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ilarity 95.5%;
Conservative
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les 105; Conserv
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                           106;
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Best Local S:
Matches 105,
                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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A; Wolecule, type: protein
A; Wolecule, type: protein
A; Residues: 1-96, K', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 < SCH
A; Net: this sequence has the Gim(3) and Gim(non-1) markers
R; Call, W. E.; Edelman, G.M.
Biochemistry 9, 1388-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfice
A; Reference number: A90655; MUID: 7,064027
A; Contents: annotation; disulfide bonds
R; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seylers' Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Totosa-Seylers' GBB:120085
A; Contents: annotation; disulfide bonds
C; Generics:
A; Gene: GBB:120085
A; Contents: annotation; disulfide bonds
A; Title: Rule of antibody structure subunit consists of two identical light (kap
A; Totosa-references: GBB:120085
A; Gene: GBB:120085
A; Totosa-references: GBB:120087
A; Totosa-referen
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C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S69399; S12664
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 34-60, 1995
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A; Reference number: S69339; MUD:95262687
A; Reference number: S69339; MUD:95262687
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-374 < KHA>
A; Residues: L-374 < KHA>
A; Cross-references: EMBL:X81695
B; Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
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A;Residudes: 1-140, CC',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%; Score 568; DB 1;
96.4%; Pred. No. 4.3e-50;
Live 2; Mismatches 2;
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No. 5e-50;
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Best Local Similarity 96.47
Matches 106; Conservative
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GSHUMI
IG gamma-3 heavy chain disease proteins - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C; Accession: A90442; A92219; A90198; A93915; A02149
R; Frangione, B.; Rosenwasser, E.; Preili, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A; Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 hea
A; Reference number: A90442; MUID:81021548
A; Contents: heavy chain disease protein Wis
A; Contents: heavy chain disease protein Wis
A; Contents: heavy chain disease protein Wis
A; Reference number: A90442
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interch
A; Note: the sequence of residues 42-76 was taken from the reference that follows
A; Michaelsen, T. E.; Frangione, B.; Franklin, E.C.
A; Michaelsen, T. E.; Frangione, B.; Franklin, E.C.
A; Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplicat
A; Reference number: A92219; MUID:77118561
A; Reference number: A92219; MuiD:77118561
A; Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A90198
A; Molecule type: protein
A; Nolecule type: protein
A; Note: this protein lacks most of the V region, all of the CH1 region, and part of t
B; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood,
Proc. Natl. Acad. Sci. U.S. A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti
A; Reference number: A33915; MUID: 82247835
A; Contents: heavy chain disease protein Omm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gaidue segment (12-28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in R; Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A; Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the Reference number: A90198; MUID:77021516
A; Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: A93915
A; Molecule type: mRNA
A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
C; Comment: The heavy chain disease protein Wis is shown.
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                                                 158 APELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 217
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
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                                                                                                                                                                           Length 289;
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Pred. No. 7.5e-50;
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us-09-674-857-6.rpr

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A.Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
Asiperfamily: immunoglobulin c region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-65/Domain: immunoglobulin homology <IM2>
F;33-302/Domain: immunoglobulin homology <IM2>
F;33-302/Domain: immunoglobulin homology <IM3>
F;34-35.14(0-200,246-304/Disulfide bonds: #status experimental
F;27-33,140-200,246-304/Disulfide bonds: interchain (to heavy chain) #status experimental
F;20-30-306/Domain: immunoglobulin homology <IM3>
F;40-200,246-304/Disulfide bonds: interchain (to heavy chain) #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
A; Molecule type: DNA
A; Residues: 1-326 < CELL>
A; Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A; Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A; Note: Lys-326 is probably removed posttranslationally
B; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an A; Reference number: A92809; MUID:81007873
A; Contents: myeloma protein Til
A; Accession: A92809
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: protein A Molecule trp-156 is at one the complement-binding site R Connell, G.E.; Parr, D.M.; Hofmann, T. Can. J. Biochem. 57, 758-767, 1979
A; Fitle: The amino acid sequences of the three heavy chain constant region domains of A; Reference number: A90752; MUID:80001357
A; Contents: Myeloma protein Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A00752
A; Molecule type: protein
A; Residues: 1-24, Fu. 7.56-57, EV', 60-85;132-171, 222',175, B',177-193, D',195-196, 'Q',1
A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A.Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli
A.Reference number: A93132; MUID:80114419
A.Contents: Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rilistein, C.; Frangione, B. Bocchen. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2. A;Reference number: A90253; MUID:72033500
A;Reference number: A90253; MUID:72033500
A;Contents: annotation; myeloma protein Sa, disulfide bonds
B;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G. A;Reference number: A91315; MUID:69064124
A;Contents: annotation; Sa, disulfide bonds
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Pred. No. 3e-47;
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A; Residues: 238-275 <HOF>
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, Mč
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Best Local Similarity
Matches 100; Conserv
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A; Note: 1493.33-14932.33
A; Nap position: 1493.33-14932.33
A; Map position: 1493.33-14932.33
A; Introns: 99/1; 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin c region; immunoglobulin homology C; Superfamily: immunoglobulin homology city. Sp9-110/Region: immunoglobulin homology city. F; 20-85/Domain: immunoglobulin homology city. F; 240-307/Domain: immuno
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Cispecies: Homo sapiens (man)
Cibate: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
CiAccession: A93906; A92809; A90752; A93132; A02148
Riellison, J.: Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A.Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-327 <ELL>
A; Note: the sequence was determined from the germline gene
A; Note: the sequence was determined from the germline gene
R; Pink, J. R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant
A; Reference number: A90249; MUID:70207560
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C.Jacestes Dept-1982 #text_change 16-Jul-1999
C.Jacession: A90933; A90249; A0150
R.Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A.;Tille: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A.;Reference number: A90933; MUID:83157104
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                                                                                 Gaps
                               1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREEQFINSTYRVVSVLTYLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 220
                                                                                                                                                                                                      61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                       Length 327;
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Pred. No. 2.4e-47;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-4 chain C region - human C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%;
ilarity 91.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 1-30;81-326 <PIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A90933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: IGHG4
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Best Local Simi
Matches 101;
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Ribrueggemann, M. (1974) 1988
A; Files Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A; Reference number: PS0017: MUID:89232738
A; Recession: PS0018
A; Molecule type: DNA
A; Residues: 1-333 < RRUD
R; Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H. Rybro. Natl. Acad. Sci. US.A. 83, 6075-6079, 1986
A; Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse a Reference number: A25941; MUID:86287397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Id gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Decise: 21:Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: Id7162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3555-3573, 1994
A;Fitle: Five putative subclasses of swine IgG identified from the cDNA sequence number: Id7158; MUID:95015845
A;Accession: Id7162
                                                                C;Species: Rattus norvégicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
C;Accession: PS0018; B25941
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A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 PELLGGPSVFIFPPRPKPILLISQNAKVTCVVVDVSEEBDDVQFSWFVNNVEVHTAQTQP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 96/1; 117/1; 227/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 REEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: IgC4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
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Pred. No. 4.1e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: immunoglobulin F; 20-82/Domain: immunoglobulin homology < IMM>
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75.2%;
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                                   Ig gamma-2b chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: B25941
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 227-333 <BR2>
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Best Local Similarity
Matches 82; Conserv
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                                                                                                                                                                                          Iggamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
C;Accession: 147160
R;Kacskovics, I:; Sun, J:; Butler, J.E.
J: Immunol: 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a sA;Reference number: 147158; MUID:95015845
A;Accession: 147160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C;Genetics: 19G2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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(Species: Sus scrofa domestica (domestic pig)

(Species: Sus scrofa domestica (domestic pig)

(Spacession: 147159

(Racskovics, 1.; Sun, 7; Butler, J.E.

J. Immunol. 153, 356-3573, 1994

A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a shacesence number: 147159; MUID:95015845

A; Accession: 147159

A; Accession: 147159

A; Accession: 147159

A; Accession: 147159

A; Conecule type: mRNA

A; Residues: 1-328 < ACC>
A; Conecule conecu
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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174 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 NSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
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79.8%; Pred. No. 2e-39;
iive 12; Mismatches 9
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Matches 83; Conservative
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C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon 0.3-Mar-1989 #text_change 21-Jan-2000
C.Accession: C.30554
A.Tamunool. 142, 708-711, 1989
A.Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A.Reference number: A.30554; MUID:89093962
A.Recession: C.30554
A.Status: pre-liminary; not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-308 <-FOLD.
C.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Superfamily: immunoglobulin homology <-IMM>
F.113-182/Domain: immunoglobulin homology <-IMM>
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Matches 83; Conservative
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A; Residues: 4-68 <BIR>
R; Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A; Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami
A; Reference number: A90359; MUID:71058486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 69-133;312-329 <TUR>
R; Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A; Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A; Reference number: A90384; MUID:75036072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Accession: A90384
A Molecule type: protein
A; Molecule type: protein
A; Residues: 134-226 < 4TRA>
B; Trischmann, T.M.; Cebra, J.J.
B) Biochemistry 13, 4804-4811, 1974
A; Title: Primary structure of the C-H3 homology region from guinea pig 1gG2 antibodies.
A; Reference number: A90385; MUID:75036073
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A. Contents: annotation; disulfide bonds
A. Note: Cys-16 is involved in a heavy-light chain bond
A. Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C. Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C. Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k. hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into C. Superfamily: immunoglobulin c region; immunoglobulin homology
C. Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: immunoglobulin homology x.M1>
                                                                                                                                                                                                                                                                                                                                  RiBirshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
Akittle: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III.
Akeference number: A90352; MUID:71058471
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A;Accession: Lype: protein
A;Residues: 27-311 -TR2>
B;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
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F;142-202/Disulfide bonds: *status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) *status experimental
F;248-308/Disulfide bonds: *status experimental
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A: Reference number: A94553
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Sequence 55,
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Sequence 43,
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Sequence 38,
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
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   Sequence 11, 18 Sequence 7, M Sequence 7, M Sequence 12, 18 Sequence 16, 18 Sequence 16, 18 Sequence 11, 18 Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Sequence 45 Application US/08761277A

Sequence 45 Application US/08761277A

Father No. 59723A:

GENERAL IMPORMATION:

TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And TITLE OF INVENTION: Leukemia

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montpomery Street, Suite 2200

CITY: San Francisco

STREET: California

COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 585; DB 2;
100.0%; Pred. No. 2.2e-62;
ive 0; Mismatches 0;
US-09-180-100-11

US-08-236-311-7

US-08-1457-311-7

US-08-140-100-22

US-09-131-247-14

US-09-131-247-14

US-09-131-247-14

US-09-131-247-14

US-09-131-247-14

US-09-131-247-14

US-08-1386-12

PCT-US95-03866-12

PCT-US95-03866-14

PCT-US95-03866-14

PCT-US95-10043-11

PCT-US95-10043-11

US-08-397-411-7

US-08-397-411-7

US-08-397-411-7

US-08-458-516-13

US-08-679-397-2
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PILING DATE: 06-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/644,664
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: GENITOPE-02406
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 377 amino acids
amino acid
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Best Local Similarity 100.
Matches 110; Conservative
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      350
3371
3371
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388
3386
3396
424
424
424
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MOLECULE TYPE: protein
US-08-761-277A-45
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TRANSFERRIN RECEPTOR SPECIFIC ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

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TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR ITLIE OF INVENTION: CONJUGATES TITLE OF SEQUENCES: 46 CORRESPONDENCE ADDRESS: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: U6-MAY-1994
CLASSIFICATION 530
PRIOR APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: CF-NOV-1991
PRIOR APPLICATION NUMBER: CF-NOV-1991
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: U7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: U7-SEP-1990
ATPONENTY/AGENT INFORMATION:
ANAMERICATION NUMBER: US 07/404,089
FILING DATE: U7-SEP-1990
ATPONENTY/AGENT INFORMATION:
                                                                           Sequence 38, Application US/08232246A Patent No. 6329508 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                            STREET: Two Mil CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                        USA
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: US
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-246A-38
                                                           US-08-232-246A-38
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                                                                                                                                                                                                                                   Phillip M.
TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
161 APELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                      RESULT 2
US-08 444-644-38
Sequence 38, Application US/08444644
Sequence 38, Application US/08444644
Patent No. 601555
GENERAL INFORMATION:
TITLE OF INVENTION: Phillip M.
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DI.
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brock, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 570; DB 3;
Pred. No. 2.7e-61;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
ATTORNEY/AGENT INFORMATION:
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98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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STATE: MA
COUNTRY:
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Best Local Si
Matches 108;
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Pred. No. 2.7e-61;
0; Mismatches 2;
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/POCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/08444644
Patent No. 6015555
GENBERL INFORMATION:
APPLICANT: Friden, Phillip M.
                                                                                                                                                                                                                            97.4%;
                                                                                                                                                         protein
internal
                                                                                                                                                                                                                                                      Conservative
                                                                                                                               amino acid
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 108; Conserv
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E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
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                                                                                                                  ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wagner, Richard W. REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                STREET: TWO ...
                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-539D-55
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                                                                                                     COUNTRY:
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ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
CONJUGATES
                 TRANSFERRIN RECEPTOR SPECIFIC
ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                      E: Hamilton, Brook, Smith & Reynolds, P.C Two Militia Drive
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 568; DB 3; Lo
Pred. No. 4.7e-61;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALK88-15AAAZ
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION 1243
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-UUL-1994
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1980
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-232-246A-21
Sequence 21, Application US/08232246A
GENERAL 10. 6329508
TITLE OF INVENTION: TRANSFERRIN RECE
TITLE OF INVENTION: ANTIBODY NEUROPE;
TITLE OF INVENTION: ANTIBODY NEUROPE;
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                          CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.1%;
Best Local Similarity 96.4%;
Matches 106; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 amino acids
TITLE OF INVENTION: TRAN
TITLE OF INVENTION: ANTI
TITLE OF INVENTION: CONJ
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-444-644-21
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
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                                                                                                                                         STREET: Two Mil!
                                                                                                                                                                                                        USA
                                                                                                                                                                              STATE: MA
COUNTRY: US,
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ropology:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.1%; Score 568; DB 4; Length 110; Best Local Similarity 96.4%; Pred. No. 4.7e-61; Matches 106; Conservative 2; Mismatches 2; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                  FILING DATE: 04-MAY 1994
CLASSIFICATION: 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION UNBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTON: IGE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
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2617-B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                  NAME: Perkins, Patricia A.
REGISTRATION UNDRER: 34,693
REPERENCE/DOCKET NUMBER: 2612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                              .... 4
....rorH: 212 amino acids
TYPE: amino acids
TOPPLOGY: lin-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.44
Matches 106; Conservative
                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                               ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IGG1 FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-620-694A-4
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Sequence 4, Application US/08430633

Patent No. 5736286

GENERAL INFORMATION:
APPLICANT: ALDERSON, MARK
APPLICANT: ACHEN, JEFREY
APPLICANT: COHEN, JEFREY
APPLICANT: PARRAH, THERESA
APPLICANT: PARRAH, THERESA
APPLICANT: PARRAH, THERESA
APPLICANT: PARRAH, THERESA
APPLICANT: TARRAH, THERESA
APPLICANT: FARRAH, THERESA
APPLICANT: PARRAH, THERESA
APPLICANT: SPRIGGS, MELANIE
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
COTTY: SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 APELLGGPSVFLFPPKPKDTLMISNTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/430,633
FTLING DATE: 28 APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.1%; Score 568; DB 2
96.4%; Pred. No. 5e-61;
tive 2; Mismatches
                SOFTWARE: WINPALLIA, F. COLONIA, CORRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/23,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION NUMBER: 07/744768
FILING DATE: 14-AuG-1991
ATTONNEY, AGENT INFORMATION:
NAME: SYODOGA, CRAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 90718P3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESS:
ADDRESS:
ADDRESS:
ADDRESS:
ADDRESS:
TEST: IMMUNEX CORPORATION
CITY: SEATTLE
STATE: WASHINGTON
COUNTY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR PAPLICATION DATA:
APPLICATION NUMBER: 08/235,397
FILING DATE: 04/28/94
                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 116 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 96.48
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: Linear
US-08-232-539D-55
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                     14 APELLGGPSVFLFPFRFKDTLMISTRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yao, Zhengbin
APPLICANT: Sprigs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                           74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
   Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA.

ZIE: 98101
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: ZI MARCH 1996
CLASSIFICATION DATA:
APPLICATION UNBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
TILING DATE: 23 MARCH 1995
97.1%; Score 568; DB 1; Lv 96.4%; Pred. No. 1.1e-60; tive 2; Mismatches 2;
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΜĀ
                                                                                                                                           US-08-936-854-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                              CLONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                    14 APELLGGPSVFLFPPKKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGYEVHNAKTK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ALDERSON, MARK
APPLICANT: ALDERSON, MARK
APPLICANT: COHEN, JEPFREY
APPLICANT: COMEN, JEPFREY
APPLICANT: COMEN, MICHAEL
APPLICANT: COMEN, MICHAEL
APPLICANT: FARRAH, THERESA
APPLICANT: FARRAH, THERESA
APPLICANT: SPRIGGS, MELANIE
TITLE OF INVENTION: That Bind MHC Class II Beta Chains
UNBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: IMMUNEX CORPORATION
STREET: SEATTLE
CITY: SEATTLE
CITY: SEATTLE
STATE: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                          .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
                                                                                                                                                                                                                                                                                                                 Length 212;
                                                                                                                                                                                                                                                                                                            Score 568; DB 2; Length 21
Pred. No. 1.1e-60;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Apple Operating System 7.1 SOFTWARE: Microsoft Word for Apple, Version 5.1a CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,633
FILING DATE: 28-APR-1995
APPLICATION UNBER: 08/235,397
FILING DATE: 04/28/94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08936854 Patent No. 5925734 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)283-0644
TELEFAX: (206)233-0644
                                                                                                     not relevant
                                                                                                                                                                                                                                                                                                          97.18;
96.48;
                   INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
                                                          LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 96.45
Matches 106; Conservative
                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                      linear
                                                                                                                                                                                ORGANISM: Human

IMMEDIATE SOURCE:

CLONE: IgG1 FC

US-08-620-694A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98101
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-936-854-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                               14 APELLGGPSVFLFPFRPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTK 73
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Sequence 4, Application US/0902255
Sequence 4, Application US/09022255
Sequence 10: 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                            74 PREEQINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
                                                                                                                                                                                                                  Score 568; DB 2; Length 212;
Pred. No. 1.1e-60;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
APPLICATION NUMBER: US/09/022,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant
                                                                                                                                                                                                                    Query Match 97.1%;
Best Local Similarity 96.4%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEC ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                     ORGANISM: Human
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Immu
STREET: 51 Univ
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206)
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                              14 APELLGGPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73
                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/0902253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                        97.1%; Score 56%; DB 3; Length 212; 96.4%; Pred. No. 1.1e-60; ive 2; Mismatches 2; Indels
      Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Apple, Version 6.0.1 CURRENT APPLICATION NUMBER: US/09/022,253
  97.1%; Score 568; DB 3; I
96.4%; Pred. No. 1.1e-60;
ive 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 6096305 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2617-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: PERKIGS, PARTICIA Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION IRFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: NO. 6096305 R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                            Best Local Similarity 96.49
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 96.4
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Human
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MEDIUM TYPE: Floppy
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                        Similarity
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CLASSIFICATION:
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CLONE: IGG1 FC
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STATE:
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      Query Match
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APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Fansion, william
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREDT: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                        74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
                                                                                                                                                                                                                                                                                  61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                          Score 568; DB 3; Length 212;
Pred. No. 1.1e-60;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDLUM TYPE: ELOPPY disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
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APPLICATION NUMBER: USSN 08/410,53
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 24,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09022696
Patent No. 6072037
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TYPE: amino acid
STRANDEDNESS: not relevant
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                                                                                                          Query Match 97.1%;
Best Local Similarity 96.4%;
Matches 106; Conservative
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human
; IMMEDIATE SOURCE:
; CLÖNE: 1gG1 FC
US-09-022-696-4
; IMMEDIATE SOURCE:
; CLONE: IgG1 FC
US-09-022-255-4
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ZIP: 98101
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TELEFAX: (
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US-09-022-696-4
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                                     14 APELLGGPSVFLFPFRPKDTLMISTRTPEVTCVVVDVSHEDPEVKFN#YVDGVEVHNAKTK 73
                1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                             61 PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 110
                                                                                                                      74 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
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96.4%; Pred. No. 1.1e-60;
"Micmatches 2;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
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APPLICATION NUMBER: US/09/022,260
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
                                                                                                                                                                                                                               Sequence 4, Application US/09022260 Patent No. 6100235
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MEDIUM TYPE: Floppy disk
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Best Local Similarity
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STATE: WA
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1 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTK 60
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APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Miliam
TITLE OF INVENTION No. 6191104el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
97.1%; Score 568; DB 4; Length 212; 96.4%; Pred. No. 1.1e-60; Live 2; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 6.0.1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
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                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
                                                                                                                                          ; Sequence 4, Application US/09022259; Patent No. 6191104; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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ATTORNEY/AGENT INFORMATION:
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amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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Best Local Similarity
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Search completed: June 21, 2002, 08:32:15 Job time: 89 sec

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TRANSFERRIN RECEPTOR SPECIFIC ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT CONJUGATES
  Sequence 4, A Sequence 5, A Sequence 50, A Sequence 33, Sequence 2, A Sequence 43, Sequence 43, Sequence 43, Sequence 43, Sequence 43, Sequence 43, Sequence 11, Sequence 11, Sequence 11, Sequence 22, A Sequence 22, A Sequence 22, A Sequence 23, Sequence 23, A Sequence 23, A Sequence 22, A S
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Two Militia Drive
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SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
US-09-022-260-4
US-09-022-259-4
US-09-022-257-4
US-08-131-247-6
US-09-131-247-6
US-09-131-247-6
US-09-138-391B-33
US-09-138-391B-33
US-09-138-869-2
US-08-459-512-43
US-08-459-512-43
US-08-466-465-8
PCT-US92-02050-43
US-08-456-100-11
US-08-457-91B-7
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ER: ALK88-15AAAZ
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: 0S 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA: DCT/US90/05077
FILING DATE: 07-SEP-1990
PRICR APPLICATION DATA: 0S 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/08444644
Patent No. 6015555
REGERRAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN I
TITLE OF INVENTION: CONJUGATES
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wagner, Richard W. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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US-08-444-644-30
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       June 21, 2002, 08:32:15; Search time 77.71 Seconds (Without alignments) 34.261 Million cell updates/sec
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                                                                                                                                                                                                                                                                                              1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPAPIEKTISKTK 109
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                                                 Compugen Ltd
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US-08-477-460B-2
US-08-379-516-2
US-09-329-916-2
US-09-409-006A-2
US-09-409-07422-2
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US-08-656-586-9
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US-08-620-694A-4
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                                             Run on:
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STREE: 30 ROCKEFELLER PLAZA
CITY: New YORK
STAME: New YORK
COUNTRY: USA
IP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILD PATA:
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STRRET: 30 ROCKefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-477-460B-2
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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US-08-477-460B-2
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TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
CORRESPONDENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                           Gaps
                                                                                                                                                                                                    1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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                                                                                                           Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 04-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Màtch
100.0%; Score 583; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.5e-60;
Matches 109; Conservative 0; Mismatches 0;
                                                                                                           Query Match
100.0%; Score 583; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.5e-60;
Matches 109; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERNCE/DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26 NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-232-246A-30

Sequence 30, Application US/08232246A

Sequence 30, Application US/0823246A

Patent No. 6329508

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 109 amino acids amino acid
    protein
internal
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FRAGMENT TYPE: internal
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-444-644-30
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Sequence 2, Application US/08477460B
Patent No. 6034223
GENERAL INFORMATION:
APPLICANIT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PERTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF ö 1 APPVAGPSVFLFPPKRPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60 Query Match
100.0%; Score 583; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 8.6e-60;
Matches 109; Conservative 0; Mismatches 0; Indels REEQFINSTFRUVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109 61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109 TELECATION UNBER: US/08/477,460B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
PRIOR PEPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-JUG-1992
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-950
TELERX: 42253 COOP UI
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARRACTERISTICS:
LENGTH: 432 amino acids

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 583; DB 4; Length 432; 100.0%; Pred. No. 8.6e-60; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08485372A

Sequence 2, Application US/08485372A

GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 37690-II-A TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400 TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEX: (212) 977-9809
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
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Matches 109; Conservative
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                                                                                                                                                                                                                                                        ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-09-329-916-2
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                                                                                                                                                                                                              MOLECULE TYPE: protein ORIGINAL SOURCE:
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STRANDEDNESS:
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STATE:
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                                                                                                                APPLICANT: Allaway, Graham P.
APPLICANT: Allaway, Graham P.
APPLICANT: Allaway, Graham P.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: No. 608478-Peptidyl Molety-Conjugated CD4-Gamma2 and CD4-IgG2
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/O8/379,516
CURRENT FILING DATE: 1996-06-10
EARLIER FILING DATE: 1996-06-10
EARLIER FILING DATE: 1992-08-07
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
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APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF
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100.0%; Pred. No. 8.6e-60;
ive 0; Mismatches 0;
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REGISTRATION NUMBER: 28,678
RECIENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
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SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
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FILING DATE: 07-AUG-1992
ATTORNEY AGENT INFORMATION:
NAME: Whith
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CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/477,460
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 07/927,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: USA ZIP: 10112 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                              Sequence 2, Application US/08379516 Patent No. 6083478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-329-916-2; Sequence 2, Application US/09329916; Patent No. 6177549
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Best Local Similarity 100.
Matches 109; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Homo sapiens
US-08-379-516-2
                                                                                                         GENERAL INFORMATION:
                                   US-08-379-516-2
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61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109

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; CELL TYPE: lymphocyte US-08-485-372A-2

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Sequence 2, Application PC/TUS9307422
GENERAL INPRMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION:
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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277 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 325
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1077-950
TELECOMMUNICATION
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
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STRANDEDNESS: unknown
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PCT-US93-07422-2
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Patent No. 6342586
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
ATILE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
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                                                                                                                               Gaps
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                                                             Length 432;
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                                                          Query Match 100.0%; Score 583; DB 4; Best Local Similarity 100.0%; Pred. No. 8.6e-60; Matches 109; Conservative 0; Mismatches 0;
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TELEFAX: (212) 977-9809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
PRIOR APPLICATION OF WISH
RIGHT SPELCATION NUMBER: US/09/1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISFRATION NUMBER: 28,678
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Best Local Similarity
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STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-409-006A-2
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Sequence 4, Application US/09329916
Patent No. 6177549
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                            1 APPVAGPSVFLFPPKPKDTLMISRTPEVICVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                            Length 530;
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                                                                                                                                                                                                                  Indels
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/477,460
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/77,931
FILING DATE: 07-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: (212) 977-9809
                                                                                                                                                                     100.0%; Score 583; DB 3;
100.0%; Pred. No. 1.1e-59;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9560
TELEEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 530 amino acids TYPE: amino acid
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4.
LENGTH: 530
                                                                                                                                                                                              Best_Local Similarity 100. Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE: lymphocyte US-09-329-916-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                    ; ORGANISM: Homo sapiens
US-08-379-516-4
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US-09-329-916-4
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                                                                  TYPE: PRT
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Sequence 4, Application US/08379516

Sequence 4, Application US/08379516

Sequence 4, Application US/08379516

Sequence 4, Application US/08379516

SEREAL NO SOBSTATE OF TAIL OF TAIL OF TAIL OF TAIL OF TAIL OF INVENTION: Immunoconjugates and Uses Thereof

FILE REFERENCE: 41215-A-PCT-US

CURRENT APPLICATION NUMBER: US/08/379,516

CURRENT APPLICATION NUMBER: US/08/379,516

CURRENT APPLICATION NUMBER: PCT/US93/07422

EARLIER FILING DATE: 1996-06-10

EARLIER FILING DATE: 1993-08-06

EARLIER FILING DATE: 1992-08-07

NUMBER OF SEQ ID NOS: 9
NON-PEPTIDYL MOIETY-CONJUGATED
CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9509
TELEX: 42253 COOP UI
INFORMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acids
STRANDENESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 583; DB 3;
Pred. No. 1.1e-59;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                COUNTY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,460B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, JOHN P.
REGISTRATION NUMBER: 28,678
                                                                                    ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: homo sapien
CELL TYPE: lymphocyte
                                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA ORIGINAL SOURCE:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                     STREET: 30 Rocker
CITY: New York
STATE: New York
                                                                                                                                                                          USA
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Sequence 4, Application PC/TUS9307422
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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Pred. No. 1.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41215-A-PCT/JPW/AJM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-LOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 977-950
TELEFAX: (212) 977-950
TELEFAX: (212) 977-950
TELEFAX: (212) 977-950
TELEFAX: (212) 977-950
TELEPAX: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                      Sequence 4, Application US/09409006A
Patent No. 6342586
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL TYPE: lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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PCT-US93-07422-4
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                                               Gaps
                                                                                                     1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
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                                                                                                                                                                                                             Indels
                                               Indels
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Patent No. 618748
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                    Pred. No. 1.1e-59;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 583; DB 4;
100.0%; Pred. No. 1.1e-59;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOAPY disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIR Release #1.24
CURRENT APPLICATION DATE
APPLICATION NUMBER: US/08/485,372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION UNBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
100.08; FI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 530 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 109; Conservative
                    Best Local Similarity 100.
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CELL TYPE: lymphocyte US-08-485-372A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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STATE: New York
COUNTRY: USA
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
STREET: 118
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Cooper & Dunham

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TOPOLOGY:
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| Patent No. 5944112
| GENERAL INFORMATION:
| APPLICANT: Bediar, Martin M. APPLICANT: Bediar, Martin M. APPLICANT: Gross, Cordell E. TITLE OF INVENTION: ANTI-CD18 ANTI-C
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: PCT/US93/07422

FILING DATE: 19930806

CLASSIFICATION: PRT/US93/07422

FILING DATE: 19930806

CLASSIFICATION: DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNEY/ABENT INFORMATION:

NAME: White, John P. REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM

REGISTRATION NUMBER: 41215-A-PCT/JPW/AJM

TELEPOMUNICATION INFORMATION:

TELEPAX: 42253 COOP U:

TELEPAX: 42253 COOP U:

SEQUENCE CHARACTERISTICS:

LENGTH: 530 amino acids

TYPE: amino acid

STRANDEDNESS: unknown
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STRÉET: 30 Rockefeller Plaza
CIȚY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: homo sapien
CELL TYPE: lymphocyte
PCT-US93-07422-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                      STATE: Ne
COUNTRY:
ZIP: 1013
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US-08-788-800-12
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CURRENT APPLICATION DATA:

APPLICATION UNMER: US/08/788,800

FILING DATE: 22-Ja4

FILING DATE: 22-Ja4

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION UNBER: P09871

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELERAX: 910/371-7168

TELERAX: 910/371-7168

TELERAX: 415/952-994

TELERAX: 415/952-994

TELERAX: 910/371-7168

INFORMATION FOR ESQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH 450 amino acids

TYPE: Amino Acid

TYPE: Amino Acid

TYPE: Amino Acid

COPOLOGY: Linear

US-08-788-800-12

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AACHORINGE TELEPROTICES O; Indels O; In
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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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110: /SIDS1/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
111: /SIDS1/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
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116: /SIDS1/gcgdata/hold-geneseqy-embl/AA1992.DAT:*
117: /SIDS1/gcgdata/hold-geneseqy-embl/AA1992.DAT:*
118: /SIDS1/gcgdata/hold-geneseqy-embl/AA1999.DAT:*
119: /SIDS1/gcgdata/hold-geneseqy-embl/AA1999.DAT:*
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583
1 APPVAGPSVFLFPPKPKDTL......CKVSNKGLPAPIEKTISKTK 109
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                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747574 segs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|                 |        | Description       | Undefined ORF2 enc | Amino acid sequenc | Human IgG2. Homo | Human IqG2 Fc reqi | Human immunoglobul | Human IL-2/Ig fusi | CD4-gamma2 chimeri | CD4-qamma 2 chimer | Human CD4-gamma 2 | Human CD4 -gamma2 c | CD4-gamma2 chimeri |
|-----------------|--------|-------------------|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|---------------------|--------------------|
|                 |        | OI .              |                    | AAB07476           | AAB67203         | AAB76423           | AAE02643           | AAY06895           | AAR26782           | AAR46678           | AAY85079          | AAB80883            | AAB67322           |
| <del>,,</del> , |        | DB :              | 14                 | 21                 | 22               | 22                 | 22                 | 20                 | 13                 | 15                 | 21                | 22                  | 22                 |
|                 |        | Length            | 109                | 217                | 217              | 217                | 326                | 381                | 432                | 432                | 432               | 432                 | 432                |
|                 | Query  | e Match Length DB | 100.0              | 100.0              | 100.0            | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0             | 100.0               | 100.0              |
|                 |        | Score             | 583                | 583                | 583              | 583                | . 583              | 583                | 583                | 583                | 583               | 583                 | 583                |
|                 | Result | No.               | г                  | 7                  | m                | 4                  | S                  | , 6                | 7                  | 80                 | 6                 | 10                  | 11                 |

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| Human 19G2 chain C The heavy chain of Human ised 323/A3 ( Human ised 323/A3 ( Human ised 323/A3 ( Human ised 225/A3 ( Human ismunoglobul The heavy chain of CD4-19G2 chimeric Human CD4-19G2 chimeric Human 19G2 chimeric PH52-8.0 humanised The heavy chain of A33 chimeric recep 233G237Az chimer Heavy chain consta Mutated CH2 sequen Mutated CH2 sequen Mutated CH2 sequen A34 (Chimeric) hum SA2 (Chimeric) hum SA4 (Chimeric) hum Amino acid sequency Human 19G3 Fc regi Immunoglobulin C-g Human 19G3 Fc regi Immunoglobulin C-g                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 5. amplify; murine; pAH4625; region; anti-human; pAH4807; capillary; pAH4808; gamma-2; ceutical; gamma-3; gamma-4; epilepsy; monoclonal; SP2/0 cell.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| AAB72230 AAY93734 AAB26884 AAB26884 AAY93701 AAY93701 AAY93707 AAY93703 AAY14996 AAW14994 AAW14994 AAW14994 AAW14994 AAW14994 AAW14994 AAW14994 AAW1745 AAX54297 AAX54297 AAX54297 AAX54297 AAX54297 AAX54297 AAX54297 AAX54296 AAW14933 AAW14934 AAW14934 AAW14994 AAW17455 AAW373755 AAW373755 AAW3737567                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | asmid pAH462; rimer; PCR; e; constant; ody; brain; neuropharma IDS; stroke; rs disease;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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Best Local Similarity 100. Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB67203;
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                                                                                                                                                                                                                                                            Query Match
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                                                                      The sequences given in AAR41707-09 are encoded by the expression vector pAH4625. This vector represents the cloning of the human gamma isotype, gamma-2, with the variable region of the murine monoclonal artibody 128.1. This plasmid encodes a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine source and the sequences encoding CHL, CH2 and CH3 are derived from a human source. This vector, in combination with the chimeric light chain vector, pAG4611 (see also AAQ43845), was transfected into SP2/0 cells and clones were isolated. 128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may capillary endotheds.
                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Fc region-containing polypeptides that have altered effector function due to one or more amino acid modifications in the Fc region, uspful in the treatment of cancer and allergic conditions such as
                                                                                                                                                                                                                                                                                                                                                                                           1 appvagpsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwyvdgvevhnaktkp 60
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgG antibody; light chain; Fc region; effector function; cancer; allergy; asthma; LFA-1-mediated disorder; tumour; cancer.
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 583; DB 14; Length 109; 100.0%; Pred. No. 1.1e-51; ive 0; Mismatches 0; Indels 0;
Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                61 REEQFINSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of native IgG Fc region humIgG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 22A; 132pp; English.
                                                   Disclosure, Fig 17J; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB07476 standard; protein; 217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2000; 2000WO-US00973.
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                                                                                                                                                                                                                                                                                                                                         Similarity
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                           disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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AAB07474-78 represent native IgG Fc regions. The proteins are used to produce Fc region-containing polypeptides that have altered effector function as a consequence of one or more amino acid modifications in the Fc region. The variant polypeptides are useful for treating cancer, altergic conditions such as asthma (with an anti-19E antibody), and LFA-1-mediated disorders. Where the polypeptide binds the HER2 receptor, the disorders where the polypeptide binds the HER2 benign or malignant tumour characterized by overexpression of the HER2 receptor. Such cancers include breast cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain
                                                                                                                                                                                                                                                                                                                                                                                                                                              gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer, colorectal cancer endometrial carcinoma, salivary gland carcinoma, kidney cancer, lurar cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGPSVFLFPPKPRDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 appvagpsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwyvdgvevhnaktkp 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a fusion protein, comprising a peptide ligand and an immunoglobulin (Ig) constant region multimerization domain (Ib). The hybrid molecules comprising the peptide ligands and their functional derivatives can be used in the same applications as, a peptide ligand can be used. For example the peptide ligand can bind ErbB2. The peptide ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion protein; immunoglobulin; multidimerization domain; ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 REEOFNSTFRVVSVLTVVHODWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 583; DB 21;
100.0%; Pred. No. 2.4e-51;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB67203 standard; protein; 217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000WO-US18185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   990S-0142088
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Length 217;

DB 22;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the ErbB2 binding ligands of the invention. Sequences AAB76421 - AAB76431 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, diseases of the nervous system, musculature and epithelia, e.g. nervous system damage resulting from trauma, surgapry, strokes, ischaemia, infection, metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and neuropathy associated with diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-naturally occurring peptide ligands which compete for binding human erB2 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; erbB2; HER2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy
                                                                                                                                                             Gaps
                                                                                                                                                                                                 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                  2 appvagpsvflfppkpkdtlm1srtpevtcvvvdvshedpevqfnwyvdgvevhnaktkp 61
I^{\prime}_{r} may bind to and inhibit the activity associated with a particular
                                                                                                                                                             .;
0
                                                                                                                        Length 217;
                                                                                                                                                                                                                                                                                            61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                             Indels
                                                                                                                      Score 583; DB 22;
Pred. No. 2.4e-51;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IgG2 Fc region amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Figure 2A; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      AAB76423 standard; Protein; 217
                                                                                                                      100.0%;
100.0%;
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-123048/13.
                                                                                                                      Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 AA;
                                                                217 AA;
                           target molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200101748-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo saplens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dennis MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB76423;
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human immunoglobulin G2 (IgG2) constant region mature protein. IgG2 forms a fusion protein with human erythropoietin (EPO). EPO has improved biological activity and an extended serum half life greater than 20 hours. The present invention relates to modified EPO forms such as fusion proteins comprising a Fc portion of an immunoglobulin (Ig) molecule and an EPO molecule (Fc-EPO). The Fc portion is fused covalently through its C-terminus directly or indirectly to the EPO molecule, and where the Fc portion as well as EPO portion may be modified or mutated. The invention also relates to non-lised EPO molecules which have a pattern of cysteines or disulphide bonding which is distinct from human or animal EPO. Pharmaceutical compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gillies S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             portion of an immunoglobulin molecule and a target molecule having biological activity of erythropoietin forms
                                                                                                                                                                                                                                                                                                                                                                                             Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV; vaccine; haemostatic; immunoglobulin G2; IgG2; EPO deficient disease; anaemia; renal failure; Human Immunodeficiency Virus; HIV; haematopoietic growth factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                     2 appvagpsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwyvdgvevhnaktkp 61
                                                                   1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel modified erythropoietin forms such as fusion proteins,
                                                                                                                                                       Way JC,
                                                                                                                                     61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                             Human immunoglobulin G2 constant region mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that can be treated with haematopoietic growth factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 583; DB 22;
100.0%; Pred. No. 3.8e-51;
tive 0; Mismatches 0;
   Score 583; DB 22;
Pred. No. 2.4e-51;
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sobel C,
                                                                                                                                                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 24; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rieke E,
100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                         AAE02643 standard; Protein; 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-2000; 2000WO-EP10843.
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                                                                                                                                                                                                                                                                                                                             (first entry)
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                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-367563/38
                 Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 109; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200136489-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hartmann A,
                                                                                                                                                                                                                                                                                                                          06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001
                                                                                                                                                                                                                                                                                         AAE02643;
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Gaps

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Mismatches

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Conservative

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1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
Matches 109;
                                                                61
                                                                                                                                 AAR26782
                                                                                                                        RESULT
                                                                                                                                                      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to vaccine compositions comprising a vaccine and a timed-release formulation of a cytokine or cytokine/immunoglobulin fusion protein or plasmid. The formulation or device releases the cytokine protein or plasmid at one or more temporal points subsequent to vaccine administration. The vaccines can be used for treating an autoimmune disease, an inflammatory disease, a neoplastic disease, or an immunologic disease in an inflammatory disease, an immunologic disease in an individual. The vaccines can be used to elicit immune responses against diseases such as AIDS, malaria, tuberculosis, hepatitis C, hepatitis B, cancer or influence. The methods can provide for enhancement of one or more immunologic parameters such as an antibody response, a cellular proliferative response as well as cytotoxic T-lymphocyte levels. In addition the Ig can increase the circulating half life of the cytokine. The present sequence represents a human interleukin-2 (IL-2)/Ig fusion protein.
                                                                                                                                                                                                                  Fusion protein; vaccine; cytokine; immunoglobulin; autoimmune disease; infectious disease; inflammatory disease; neoplastic disease; cancer; immunologic disease; immune response; malaria; tuberculosis; hepatitis; AIDS; influenza; interleukin; IL-2; Ig; human.
       REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                1..153
/note= "interleukin-2 (IL-2)"
154..381
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                     /note- "immunoglobulin G"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Fig 10A-E; 66pp; English.
                                                                                                                              AAY06895 standard; Protein; 381 AA
                                                                                                                                                                                              Human IL-2/Ig fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US20321
                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0990180
                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0060338
                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New vaccine compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barouch DH, Letvin NL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-254931/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX34598
                                                                                                                                                                                                                                                                                                                                                          WO9916466-A2
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1997;
                                                                                                                                                                         01-JUL-1999
                                                                                                                                                    AAY06895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                            Protein
                                                                         171
                                                    61
                                                                                                                    AAY06895
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Score 583; DB 20; Length 381; Pred. No. 4.6e-51;

100.08; 100.08;

Best Local Similarity

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It was produced by expresion of the coding mutagenised cobnergiate as described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, eg Diphtheria, Pseudomonas exotoxin A (domainS I or II) or the deglycosylated A-chain
This sequence represents a CD4-gamma2 chimeric heavy chain homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery; chimeric; increased serum half life; HIV infection; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt CD4-gamma-2} and {\tt CD4-IgG2} chimera(s) and expression vectors - for treatment, prevention and diagnosis of HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 432;
                                                                                                           REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 583; DB 13;
Pred. No. 5.4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                               CD4-gamma2 chimeric heavy chain homodimer.
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                                                                                                                                                                                                                                                                  AAR26782 standard; Protein; 432
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100.0%;
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/label= CH2
326..433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..216
/label= CD4
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maddon PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-300034/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09213947-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-1992
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Domain
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Local Similarity
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                                                                         peptidyl toxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected cells and to treat HIV infected subjects to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate comprising the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject.
       Gaps
                                                    1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV; human immunodeficiency virus; radionuclide; toxin; therapy; treatment; imaging; detection; targetting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-1gG2 immuno:conjugates - used to kill HIV-infected cells and to image and stage HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-
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                                                                                                                                                            REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
       Indels
       ٥;
    0; Mismatches
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217..325
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/label= CH2 Region.
326..432
/label= CH3 Region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..204
/label= CD4 Region.
                                                                                                                                                                                                                                                                                                 AAR46678 standard; Protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      CD4-gamma 2 chimeric heavy chain.
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Matches 109; Conservative
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N-PSDB; AAQ57750.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                              AAR46678;
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Length 432;

100.0%; Score 583; DB 15;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the target of interaction with the human immunodeficiency virus HIV. The immunoconjugate is used to kill cells infected with HIV, and for treating or preventing infection. It is also used for imaging HIV-infected tissues (for staging or prognosis of infection, and for assessing efficacy of treatments). The immunoconjugate is also used to determine the HIV envelope glycoprotein burden, once determined, this information is used in the staging and prognosis of HIV infected patients. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoproteal; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging; prognosis; envelope glycoprotein burden; human.
                                                                                               Human CD4-gamma 2 chimeric heavy chain homodimer amino acid sequence.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the human CD4-gamma 2 chimeric heavy chain
                                                                            1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to heterotetramer of CD4-immunoglobulin chimeras
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                                                                                                                                                        61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                             Indels
                Pred. No. 5.4e-51;
Mismatches 0;
                                                                                                                                                                                                                                                                                                     AA.
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100.08; PIT
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93WO-US07422.
95US-0379516.
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                                      Conservative
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06-AUG-1993;
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present invention.

homodimer. This sequence was used in the method of the

432 AA;

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immunoconjugate should be active against all strains of HIV (since the CD4-gpl20 interaction is essential for infection). The heterotetramers are assembled intracellularly and secreted efficiently from mammalian cells, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell, or treating a subject having CD4+ cells infected with HIV involves using CD4-IgG2 chimeric heterotetramer to form a complex with the HIV -
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;
immunoglobulin gamma 2.
                                                                                                                                                                                100.0%; Score 583; DB 21;
100.0%; Pred. No. 5.4e-51;
ive 0; Mismatches 0;
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92WO-US01143.
92US-0960440.
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Best Local Similarity 100.
Matches 109; Conservative
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                                                                                                                             432 AA;
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08-DEC-1992;
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                                                                                                                             Sequence
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                            Gaps
                                                                             217 appvagpsvflfppkpkdtlmisrtpevtcvvvdvshedpevqfnwyvdgvevhnaktkp 276
                                                     1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappalight chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterotetramer having two chimeric CD4-1gG2 heavy chains encoded by an expression vector CD4-1gG2HC-PRCCW and two chimeric CD4-kBCPW and expression vector CD4-KLC-PRCW, The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, for the treatment and prevention of infection with HIV.
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  Length 432;
                                                                                                                        61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                          Indels
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Pred. No. 5.4e-51;
Mismatches 0;
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 Score 583; DB 22
Pred. No. 5.4e-51
                          0; Mismatches
                                                                                                                                                                                                                                                                                                                chelator; chimeric; HIV;
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100.0%; Pr
tive 0;
100.0%;
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92US-0927931.
93US-0379516.
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                                                                                                                                                                                                                                                          (first entry)
Query Match 100.
Best Local Similarity 100.
Matches 109; Conservative
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Best Local Similarity 100.
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                Immunoconjugate;
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07-AUG-1992;
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Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Combination for treating cancer (e.g. breast, gastric or prostate cancers), or in the manufacture of a medicament for anti-cancer therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody with a chemotherapeutic agent -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised 323/A3 (IgG2cys) antibody heavy chain amino acid sequence.
                                                                                                                                                                                        61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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N-PSDB; AAF63376.
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The present sequence represents the constant region of human igG isotype 2 (IgG2, C-gamma-2). C-gamma-1 (see AAY31669) and C-gamma-3 (see AAY31671) bind Fc receptors with high affinity, whereas C-gamma-4 (see AAY31671) has 10-fold lower binding affinity and C-gamma-2 does not bind to Fc receptor gamma-1. The invention provides methods for the genetic construction and expression of antibody-based fusion proteins with enhanced circulating half-lives. The fusion proteins with enhanced circulating half-lives. The fusion proteins lack the ability to bind to immunoglobulin Fc receptors, either as a consequence of the antibody isotype used for protein construction, i.e. a C-gamma-2 constant region (FC) or a C-gamma-4 Fc receptor, or through directed mutagenesis of antibody isotypes that normally bind Fc receptors, i.e. C-gamma-1 croulating half-life of a non-lumunoglobulin (Ig) protein such as a cytokine, e.g. tumour necrosis factor (INF), an interleukin or a ligand-binding protein, e.g. CD4, CTLA-4, TNF receptor or an interleukin receptor, or a protein toxin (claimed). The fusion proteins are used to deliver selectively the second non-Ig protein can exert a localised biological effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody-based fusion proteins, used for the delivery of e.g. a cytokine, ligand-binding protein or protein toxin to target cells in
                                                                                                                                                                                                                                                 C-gamma-2; antibody; fusion protein; circulating half-life;
                                                                                                                                                                                                                                                                                                                                                              /note=""the identity of these residues is not specified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 443;
               61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 583; DB 20;
Pred. No. 5.5e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wesolowski J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 32-33; 41pp; English.
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                AAY31670 standard; Protein; 443 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0075887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LEXI-) LEXIGEN PHARM CORP.
                                                                                                                                                                                09-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                human; drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-527594/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lan Y,
                                                                                                                                                                                                                Human IgG2 chain C.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             Misc-difference 1
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                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                 AAY31670;
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Length 442;

227 appvagpsvflíppkpkdtlmisrtpevtcvvvdvshedpevqfnwyvdgvevhnaktkp 286

1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60

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100.0%; Score 583; DB 22; 100.0%; Pred. No. 5.5e-51; ive 0; Mismatches 0;

Ouery Match 100. Best Local Similarity 100. Matches 109; Conservative

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61 REEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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                                                                                                                                                                                                                                                                                                                                    Cytotoxic T-lymphocyte antigen 4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)-4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders -
                                                Gaps
                                 1 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davis CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a heavy chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)-4. Antibodies of the invention are composed of a heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient disorders.
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                                                                                                                288 reeqfnstfrvvsvltvvhqdwlngkeykckvsnkglpapiektisktk 336
                                                                                               61 REEQFINSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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   Indels
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                                                                                                                                                                                                                                                                                                       The heavy chain of immunoglobulin clone 11.2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanke JH,
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mueller EE,
                                                                                                                                                                                                            AAY93734 standard; Protein; 451 AA
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                                                                                                                                                                                                                                                                           (first entry)
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-442647/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                         03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corvalan JR;
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 109;
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                                                                                                                                                                                                                                           AAY93734;
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Combination for treating cancer (e.g. breast, gastric or prostate cancers), or in the manufacture of a medicament for anti-cancer therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody with a chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                          Anti-Ep-CAM antibody, cyclic adenosine monophosphate; cell synthesis; chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
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                                                                                                                                                                                                                                                                                                                                        Humanised 323/A3 (IgG2cys) antibody heavy chain amino acid sequence.
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100.0%; Score 583; DB 22;
100.0%; Pred. No. 5.8e-51;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; Fig 14; 103pp; English.
                                                                                                                                                                 AAB72236 standard; Protein; 461
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                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stimmel JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-182729/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200107082-A1.
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Homo sapiens.
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                                                                                                                                                                                                                                                                                10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chain.
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Matches 109;
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Local Similarity 100. nes 109; Conservative

Matches

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Search completed: June 21, 2002, 08:36:07 Job time: 321 sec

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996dx0 homo sapten
996ds0 homo sapten
996e61 homo sapten
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SEQUENCE FROM N.A.
MEDLINE-21477448; PubMed=11593034;
Hu Z., Garen A.;
Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
EMBL; AF272774; AAK58666.1; -.
EMBL; AF272774; AAK58666.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 3.5e-51;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
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87.7%;
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Q99lc4 mus musculu
Q9d8l4 mus musculu
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Q96ga6
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                          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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72.2%; Score 421; DB 11; 73.5%; Pred. No. 1e-38; ive 15; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                           463 AA.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00409; 16; 2.
SMART; SM00409; 162; 2.
SMART; SM00406; 160; 1.
SMART; SM00410; 16_11, 2.
SMART; SM00410; 16_11, 8.
SMART; SM00410; 16_11, 8.
SMART; SM00410; 16_11, 8.
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InterPro; IPR003597; Ig_c1.
                                     Best Local Similarity 73.5
Matches 75; Conservative
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Walide K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Walide K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

"Cloning of cDNas encoding for anti-white pine blister rust monoclonal artibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

BEMBL; AF152372; AAD40243.1;

RICEPTO: IPR003506; Ig_MHC.

BR InterPro: IPR003506; Ig_MHC.

BR InterPro: IRR003506; Ig_W.

BR SMART; SM00410; IG_like; 2.

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                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98383416; PubMed=9717671; Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.; Capanization of the equine immunoglobulin heavy chain constant region "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; EMBL, AJ300675; CAC44624.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                          Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.2%; Score 450; DB 6; Length 337; 74.5%; Pred. No. 4.4e-42; Live 17; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 QFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTITKTK 228
                                                                                                                                                                                                                                                                                                                            Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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Last sequence update)
Last annotation update)
              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNGGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT)
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                                                                                                                                   255 SVFIFPPREKDVLTITLTPRVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 67
                                                                                                     67
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1810060009RIX PROTEIN.
1GH-1 OR 181006009RIX.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                     8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
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Length 437;
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                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG_MHC; UNKNOWN_1.
51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 356
                                                                                                                                                                                                                                        68 TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                               68 TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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SEQUENCE FROM N.A.
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            Query Match
Best Local {
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                                         Matches
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Q99L25
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099L31
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       CRAINE-2108560; PubMed=11217851;

AMAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arawawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda T., Gissi C., King B., Kochiwa H.,
Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ruonstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Syya T., Shibata Y., Storch K.-F.,
Nordone P., Rung B., Ringwald K.H., Weitz C., Whittaker C., Wilming L.,
Whyshaw-Boots K., Roshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 AKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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9
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327, AAH10327.1; -.
Hypothetical protein.
SEQUENCE 473 AA, 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG_MHC; UNKNOWN_1.
51699 MW; 9DED57A514475FBB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 51.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003000; Ig_like.
InterPro; IPR003000; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 4.
SMART; SM00409; IG; 2.
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SMART; SM00410; IG_11ke; 1.
PROSITE; PS00290; IG_MHC; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 62.3
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          ); IG; 2.
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MGD; MGI:96443; Igh-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00409;
SMART; SM00407;
                                                                                                                                                                                                                                                                           Hayashizaki Y.;
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                                                                                                                    263 GPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDY 322
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                                                Gaps
                                                                                            6 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Length 473;
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66.6%; Score 388; DB 11; Length 4 66.3%; Pred. No. 5.6e-35; ive 17; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 DYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 NSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %; Score 380; DB 11;
%; Pred. No. 4.3e-34;
17; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003600; Ig.like.
InterPro; IPR0036006; Ig.MHC.
InterPro; IPR003596; Ig.MHC.
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65.1%;
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Best Local Similarity 65.1%
                                              69; Conservative
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                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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NCBI_TaxID=9606;
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                                                          09BQB8
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                 RESULT
Q9BQB8
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                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                       Length 473;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-LYMPH, LYMPHOMA;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004476; AAH04476.1; -.
HSSP; P01857; IFC1.
InterPro; IPR003507; Ig_c1.
InterPro; IPR003500; Ig_like.
InterPro; IPR003066; Ig_MHC.
Pfam; PF00047; Igc.1; 3.
SMART; SM00407; IGc.1; 3.
SMART; SM00407; IGc.1; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.2%; Score 380; DB 11; Length 4 Best Local Similarity 65.1%; Pred. No. 4.3e-34; Matches 69; Conservative 17; Mismatches 20; Indels
Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2001) to the EMBL, BC003888; AAH03888.1; -. HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00290; IG_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 375 AA; 41314 MW; BIAOA0998F473619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                          InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam: PP00047; Ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL 41.3 KDA PROTEIN. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.9%
Best Local Similarity 29.7%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BSZ1;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
01-DEC-2001 (FREMBLR FOR MGC:1905) (PROTEIN FOR MGC:1228).
0NKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
Elmo sapiens (Human).
Eukaryota: Metacuman).
Mammalia: Metheria: Primates: Craniata: Vertebrata: Euteleostomi: Mammalia: Butheria: Primates: Catarrhini: Hominidae: Homo.
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TISSUE=LYMPH, LYMPHOMA;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1; -.
HSSP; P01825; 7FAB.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006180; AAH06180.1; -. EMBL; BC001872; AAH01872.1; -. HSSP; P01825; TFAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
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597 AA.
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Best Local Similarity 29.74
Matches 30; Conservative
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TISSUE=RHABDOMYOSARCOMA;
     PRELIMINARY;
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SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:20337).
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                      Length 597;
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC105706.
Hypothetical protein.
SEQUENCE 597 Aa; 65039 MW; 4FCA3ADBECE263D9 CRC64;
                                                                                                                       ll protein.
597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                   426 FSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK 466
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                                                                                                                                                                     Query Match

24.9%; Score 145; DB 4;
Best Local Similarity 29.7%; Pred. No. 9.9e-08;
Matches 30; Conservative 25; Mismatches 44;
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                                  InterPro; IPR003596; Ig_v.
Pfam, PF00047; Ig; 5.
SMART; SW00409; IG; 2.
SMART; SM00407; IGc1; 4.
SMART; SM00407; IGc1; 4.
SMART; SW00410; IG_114.
SMART; SW00410; IG_11ke; 1.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                      Hypothetical
SEQUENCE 59
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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24.9%; Score 145; DB 4; Length 614;
Best Local Similarity 29.7%; Pred. No. 1e-07;
Matches 30; Conservative 25; Mismatches 44; Indels
                                                                                                                                                                                                                       Query Match 24.9%; Score 145; DB 4; Length 613; Best Local Similarity 29.7%; Pred. No. 1e-07; Matches 30; Conservative 25; Mismatches 44; Indels
                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -
SEQUENCE 613 AA, 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PRIMARY B-CELLS FROM TONSILS;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0098151; AAH09851.1; -.
SEQUENCE 614 AA; 67921 WW; S5EF536E77AA9BBB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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TISSUE=PRIMARY B-CELLS FROM TONSILS;
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Strausberg R.;
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Search completed: June 21, 2002, 08:59:31 Job time: 1630 sec

gallus gall mus musculu mus spretus heterodontu heterodontu

homo sapien

sapien qorilla gor homo sapien oryctolagus heterodontu

mus musculu

OM protein

Run on:

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TISSUE=Fetal liver;
MEDLINE=84235992; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-80001357; PubMed=113060;
Connell G.E., Parr D.M., Hofmann T.;
The amino acid sequences of the three heavy chain constant region
domains of a human IgG2 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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TSSGE-FEA1 liver;
MEDLINE-83001943; PubMed-6811139;
Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
Takahashi N., Geda S., Obata M., Nikaido T., Nakai S., Honjo T.;
Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellison J.W., Hood L.E.;
"Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human
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SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE)
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-GG gamma-2 chain C region.
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Wang A.-C., Tung E., Fudenberg H.H.;
"The primary structure of a human 1gG2 heavy evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens (Human)

NCBI\_TaxID=9606;

21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 19 gamma-1 chain C region.

330 AA.

STANDARD;

GC1\_HUMAN P01857;

GC1\_HUMAN

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REMOVED POST-TRANSLATIONALLY (PROBABLE).
S -> A (IN MYELOMA PROTEINS TIL & ZIE).
C TIG-VARD3889.
C -> S (IN REF. 3).
8310878C6878CF9C CRC64;
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                                    REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
                                                 Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
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                                                                                                                                     immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995)
                                                                                  SEQUENCE OF 1-121 (DOT).
MEDLINE=95255298; PubMed=7737190;
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MEDLINE=72033500; PubMed=4940472;
immunoglobulins gamma chains.";
dol. Immunol. 16:923-925(1979).
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InterPro; IPR003597; Ig_c1.
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Pfam; PF00047; ig; 3.
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SMART; SM00407; IGG1, 2.
PROSITE; PS00290; IG_MHC; 2.
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MEDLINE=71064024; PubMed=5489771; Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Cunningham B.A., Edelman G.M.; Waxdal M.J., Edelman G.M.; The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970).
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MEDILNE-82274238; PubMed-6287432;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
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MEDLINE-71064025; PubMed-5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
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"The covalent structure of a human gamma G-immunoglobulin. X.
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MEDLINE=77070269; PubMed=826475;
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Biochemistry 9:3188-3196(1970).
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Gaps

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100.0%; Score 583; DB 1; Length 326; 100.0%; Pred. No. 3e-52; ive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 109; Conservative

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P01861;
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                                                             "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.",
Blochemistry 2.0:2561-2370(1981).

I MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, 6 THE GIM(1) MARKER, 239-D 6 241-L. KOL 8 EU SEQUENCES HAVE THE GIM(3) MARKER, 2 THE GIM (NON-1) MARKERS.

I MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 8 272.

MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 155,166,177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 266-272.
                                                                                                                                                                                                                                                                             MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198, 2674272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Ig_ 13.
SWART; SW00410; IG_like; 1.
SWART; SW00407; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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/FIId-VAR_003886.
D -> E (IN GIM(NON-1) MARKER).
/FIId-VAR_003887.
L -> M (IN GIM(NON-1) MARKER).
/FIId-VAR_003888.
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HEAVY CHAIN).
HEAVY CHAIN).
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REMOVED POST-TRANSLATIONALLY.
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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                                X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
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HINGE.
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CH3.
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                                                   MEDLINE=81208100; PubMed=7236608;
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1FC1; 15-JUL-92.
1FC2; 15-JUL-92.
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PDB; 1FC1; 15
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MEDLINE=70207560; PubMed=4192699;
Plnk J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Blochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PP-----VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-83157104; PubMed-6299662;
Ellison J.W., Buxbaum J.W., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 AKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 AKTKPREEQYNSTYRVVSVLTVLAQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.8%; Score 535; DB 1; Length 330;
87.7%; Pred. No. 2.4e-47;
Live 5; Mismatches 3; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
1GHG4.
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PIR; A02150; G4HU.
HSSP; P01842; 7FAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frangione B., Rosenwasser E., Prelli F., Franklin E.C.; "Primary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis."; Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-77118561; Pubmed-402263;
Michaelsen T.E., Frangione B., Franklin E.C.,
Primary structure of the 'hinge' region of human 19G3. Probable
quadruplication of a 15-amino acid residue basic unit.",
J. Biol. Chem. 252:883-889(1977).
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1g-amma-3 chain C region (Heavy chain disease protein) (HDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-77021516; PUDMEd-823945; MEDIINE-77021516; PUDMEd-823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.; Wille amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoglobulin G3."; Blochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                   HEAVY CHAIN).
                                                                                                                                INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                 90.6%; Score 528; DB 1; Length 327; 92.5%; Pred. No. 1.2e-46; Live 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                         64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                   35940 MW; 3EDBD811EF208E7A CRC64;
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                                                                       Immunoglobulin domain; Immunoglobulin C region.

NON. TER 1 1 1 98 CH1.

DOMAIN 99 110 HINGE.

DOMAIN 111 220 CH2.
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MEDLINE-8,2247835; Pubmed-6808505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE-81021548; PubMed-6774747;
      InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SMO0407; IG_like; 1.
SMART; SMO0407; IG_like; 1.
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327 AA;
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P01860;
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                                                                                                                                                                                                                                                                                                                                             REF. 2.

-I MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALLO FO THE CHI REGION.

-I MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.

-I GAMMA-3 HEAVY CHAINS.

-I MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLANS.

-I MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15 RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                                                                           gene deletion model.";
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-!- SUBGUNIT: DIMER LINKED BY 12 DISCLFIDE BONDS; IT HAS AN EXTRA
-!- SUBGUNIT: DIMER LINKED BY 12 DISCLFIDE BONDS IT HAS AN EXTRA
-!- NUTERCHAIN DISCLFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLE PRESENT IN THE HINGE RECION.
-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat. DOMAIN 12 73 HINGE.
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Alexander A., Steinmetz M., Barritault D., Frangione B., Franklin E.C., Hood L., Buxbaum J.N.; "Gamma Heavy chain disease in man: cDNA sequence supports partial gene deletion model.";
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F -> Y (IN OMM).
/FTIG-VAR_003892.
T -> A (IN OMM).
/FTIG-VAR_003893.
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HSSP, P01857; IFCI.
MIM; 147120;
InterPro: IPR003505; Ig_MHC.
InterPro: IPR003507; Ig_CI.
InterPro: IPR003500; Ig_Ike.
Pfam; PP00047; ig, 2.
SMART; SM00410; IG_Like; 1.
SMART; SM00407; IGCI; 1.
PROSITE; PS00290; IG_MHC; 1.
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"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-11058474; PubMed-4922544; Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                          MEDLINE=71058471; PubMed=5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
Birsucture of heavy chain from strain 13 quinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cystine jouing heavy and light chains.";
                                                                                                            Gaps
                                                                                                                               4 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 227-311.
MEDLINE-75036073; PubMed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2 chain C region.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                            ;
0
                                                                                        Length 290;
                                                                                       Score 527; DB 1; Length 29
Pred. No. 1.3e-46;
6; Mismatches 3; Indels
                  MISSING (IN ZUC).
/FIG-VAR_003895.
F -> Y (IN OMM).
/FIG-VAR_003896.
                                                                                                                                                                               64 QFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
S -> N (IN OMM).
/FTId=VAR_003894
                                                                                                                                                                                                                                         329 AA
                                                                                                                                                                                                                                                                                                                                                                Trischmann T.M.;
Submitted (APR-1975) to the PIR data bank.
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-75036072; PubMed-4429665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 13:4804-4811(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 13:4796-4803(1974)
                                                           MW.
                                                                                       90.4%;
al Similarity 91.5%;
97; Conservative
                                                          290 AA; 32331
                                                                                                                                                                                                                                         STANDARD;
                   227
                                       279
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                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10141;
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                                       279
                  227
 227
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                                                                                                                                                                                                                                         GC2_CAVPO
P01862;
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                                                          SEQUENCE
 VARIÁNT
                   VARIANT
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                                                                                                           Matches
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-!- MISCELLANEOUS: THIS CHÁIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
13 INBRED GUINEA PIGS.
14 A02151, G20P.
15 HSSP; P01772; 2FB4.
16 InterPro; IPR003006; Ig_MHC.
17 InterPro; IPR003597; Ig_c1.
18 InterPro; IPR003500; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-84.03930; Pubmed-6313520; Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pratt D.M., Mole L.E.; "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype."; Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PP--VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig gamma chain C region.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-83299917; PubMed-6193512; M., Hood L., Knight K.L.; Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.; Heavy chain genes of rabbit 196: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes."; Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                     Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
                                                                                                                                                                                                                                                                        INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.8%; Score 436; DB 1; Length 329; 74.5%; Pred. No. 2.9e-37; ive 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               36074 MW; 5D231B7164D1FBA9 CRC64;
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SEQUENCE OF 1-128.
MEDLINE=76135469; PubMed=1243651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 18:387-397(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 88-266 FROM N.A.
                                                                                                                                                   Pfam; PF00047; 1g; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
                                                                                                                                                                                                                PS00290; IG_MHC; 1
Biochemistry 10:26-31(1971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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79
105
107
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178
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SEQUENCE OF 132-161.
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142
178
248
329 AA;
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Matches 82; Conser
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28
105
107
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PROSITE;
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CARBOHYD
DISULFID
SEQUENCE
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P01870;
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Brueggemann M.;
Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74.473-482(1988).
PIR; PS0018; PS0018.
HSSP: P01842; 7FAB.
InterPro; IPR003050; Ig_MHC.
InterPro; IPR003597; Ig_C.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SMO410; IG_like; 1.
      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.4%; Score 428; DB 1; Length 33
70.8%; Pred. No. 1.9e-36;
ive 19; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain: Immunoglobulin C region.
NON_TER
1 1 1 INTERCHAIN (WITH A
                                                                                   SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed=3149946;
                                                                                                                                                                                                                                                                     SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 70.8%
Matches 75; Conservative
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80
106
109
1112
1115
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333 AA;
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                                                      NCBI_TaxID=10116;
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P22436;
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                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PP--VAGPSVFLFPPKPPTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 59
                                                                                                                                                                          MISCELLANDOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKERS AND REF.5 THE E15 MARKER.
                                                                                                               Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
               Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit
Immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.6%; Score 429; DB 1; Length 323; 71.8%; Pred. No. 1.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T -> M (IN D11 MARKER).

N -> E (IN E15 MARKER).

V -> V (IN REF. 2).

Q -> E (IN REF. 3).

Q -> E (IN REF. 5).

N -> D (IN REF. 5).

E -> Q (IN REF. 5).

N -> D (IN REF. 5).

E -> Q (IN REF. 5).

N -> D (IN REF. 5).

N -> D (IN REF. 5).

E -> G (IN REF. 5).

N -> D (IN REF. 5).

Y -> W (IN REF. 5).
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69E8AA118D579A8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.5e
; Mismatches
                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
MEDLINE=70110015; PubMed=5461106,
                                                                                               SEQUENCE OF 129-131 AND 155-322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                Biochem. J. 116:249-259(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 N
35404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P01857; IFC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
Pfam; PF00047; Ig; 3.
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Immunoglobulin domain; Immun
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233
246
256
260
266
.280
323 AA;
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SMART;

RRYRRY RRYRY 
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Gaps

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Length 333;

CHAIN). CHAIN). CHAIN).

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                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                        MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
1g gamma-3 chain C region, secreted form.
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(Rel. 17, Created) (Rel. 17, Last sequence update) (Rel. 38, Last annotation update) chain C region.

GCB\_RAT P20761; 01-FEB-1991 ( 01-FEB-1991 ( 15-JUL-1999 ( 19 gamma-2B c

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333 AA

STANDARD;

RESULT GCB\_RAT

Best Loca Matches

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SEQUENCE (MYELOMA PROTEIN MOPC 21).
MEDLINE-78242288; PubMed-98524;
 InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                 Local Similarity 69.4%
hes 77; Conservative
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1113
223
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114
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398 AA;
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P01868;
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GC1_MOUSE
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                                                                                                                                                                                                                                                                                                                                              2 PP---VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                   3,
                                   InterPro; IPR003507; 1g_C1.
InterPro; IPR003597; 1g_C1.
InterPro; IPR003500; 1g_like.
InterPro; IPR003600; 1g_like.
SMART; SM00410; 1G_like; 1.
SMART; SM00407; 1GCl; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
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MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                        Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                      59 KPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                          36228 MW; F45827174182BAD6 CRC64;
                                                                                                                                                                                                                                                                                    Query Match 72.3%; Score 421.5; DB 1; Best Local Similarity 69.4%; Pred. No. 8.8e-36; Matches 77; Conservative 14; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-0CT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-3 chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 AA.
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HINGE.
CH2.
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EMBL F J00451; -; NOT_ANNOTATED_CDS.
PIR; B02156; G3MSC.
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EMBL; V01256; CAA24767.1; ALT_SEQ.
PIR; AQ2155; G3MSM.
HSSP; P01857; IFC1.
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SEQUENCE FROM N.A.
                            P01857; 1FC1
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ID GC3M_MOUSE
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Gaps
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MEDLINE-80012837; PubMed-113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDIZINE-80202559; PubMed-6705752;
Obbata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINRE-80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
Takahashi N., Mano Y.;
Geloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
Cell 18:559-568(1979).
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Interpro; IPR003597; Ig_c1.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
Promoty, ig; 3.
SMART; SM00407; IG_like; 1.
SMART; SM00407; IG_like; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s; Score 421.5; DB 1; Length 398;
s; Pred. No. 1.1e-35;
14; Mismatches 17; Indels 3;
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mus musculus (Mouse).
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Nucleic Acids Res. 6:3305-3321(1979)
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CH2.
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                   Q
                                                                                                                                 "The disulphide bridges of a mouse immunoglobulin G1 protein."; Biochem. J. 126:837-850(1972).
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   Adetugbo K.;
"Evolution of immunoglobulin subclasses. Primary structure of
"murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
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INVERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.2%; Score 421; DB 1; Length 324; 73.5%; Pred. No. 9.7e-36; Live 15; Mismatches 12; Indels
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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                                                                                     DISULFIDE BONDS (MOPC 21).
MEDLINE=73008889; PubMed=5073237;
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24175.1; --
EMBL; V00795; CAA24176.1; --
PIR; A02159; GIMS.
HSSP; P01842; 7FAB.
GlycoSultedB; P01868; --
MGD; MGI:96446; IGh-4.
InterPro; IPR003906; Ig_MHC.
InterPro; IPR003597; Ig_C1.
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P01869;
21-JUL-1886 (Rel. 01, Created)
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Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;

Proc. Nati. Acad. Sci. U.S.A., 79:2623-2627(1982).

Proc. Nati. Acad. Sci. U.S.A., 79:2623-2627(1982).

Proc. Nati. PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MENA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODED MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEGMENT OF MU CHAINS.
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O., "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 323-366 FROM N.A. MEDIATE-8115295; Pubmed-6799207; MEDIATE-8115295; Pubmed-6799207; Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.; "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; cell 26:19-27(1981).
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PROSTIE; PS00190; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
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cell 18:559-568(1979).
                                                                                                                 Mus musculus (Mouse).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                          Gaps
                                                                                                                                                            8 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 67
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-88166003; PubMed-3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Brueggemenn M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Sequence of a rat immunoqlobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
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                                                                                                                   Length 393;
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                                                                         CYTOPLASMIC (POTENTIAL).
4CC88343B7A1CE27 CRC64;
                                          N-LINKED (GLCNAC. . .).
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NON_TER 1 1 1 1 CH1.
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01-FEB-1991 (Rel. 17, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2c chain C region.
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HINGE.
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HSSP: P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                     43386 MW;
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Best Local Similarity 73.55
For 75, Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                  7 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 66
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013BAB45EF49B9DA CRC64;
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b; Pred. No. 1.8e-32;
17; Mismatches 15; Indels
                                                                  Length 329
                                                              69.5%; Score 405; DB 1; Length 32
69.9%; Pred. No. 4.2e-34;
ive 16; Mismatches 15; Indels
               5FCD7B7933850773 CRC64;
                                                                                                                                                                                                   67 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 109
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-1 chain C region.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                   326 AA
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HINGE.
CH2.
CH3.
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MEDLINE-89232738; PubMed-3149946;
307
36571 MW;
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68.08;
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InterPro; IPR003597; Ig_cl.
Pfam: PF00047; Ig; 3.
SMART: SM00407; IGcl.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 69.98
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PIR; PS0017; PS0017.
HSSP; P01842; 7FAB.
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326 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-81198976; PubMed-6262729; Yamawaki-Kataoka Y., Miyata T., Honjo T.; Yamawaki-Kataoka Y., Miyata T., Honjo T.; mrhe complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.; Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-81223894; PubMed-6787604; Ollo R., Auffray C., Morchamps C., Rougeon F.; Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-81076554; PubMed-6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
Structure of the constant and 3' untranslated regions of the murine
Balb/c gamma 2a heavy chain messenger RNA.";
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MEDLINE=74175517; PubMed=4831970;
Bourgois A., Fougereau M., Rocca-Serra J.;

"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";

Eur. J. Blochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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"Determination of the primary structure of a mouse gamma G2a "metermination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Biochem. 30:452-462(1972).
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NON^CTER
                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
13 gamma-2A chain C region, A allele.
Mus musculus (Mouse)
                             330 AA
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InterPro; IPR003006; Ig_MHC.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Transmembrane; Alternative splicing.
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                                                                                                                                                       Length 330;
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MW; B84361C5445A6864 CRC64;
                                                                                                                                                       66.7%; Score 389; DB 1; Length 33 ilarity 66.0%; Pred. No. 1.8e-32; Conservative 17; Mismatches 19; Indels
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01-A0G-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 Jumma-2A chain C region, membrane-bound form.
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HSSP; P01857; 1FC1.
MGD; MGI:96443; IGh-1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PR0047; Ig; 3.
SMART; SM00410; IG_like; 1.
SNART; SM00407; IG_like; 1.
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Best Local Similarity
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|          | INTERCHAIN (WITH A HEAVY CHAIN). | INTERCHAIN (WITH A HEAVY CHAIN). | INTERCHAIN (WITH A HEAVY CHAIN). |          |          | POTENTIAL. | CYTOPLASMIC (POTENTIAL). | N-LINKED (GLCNAC) (POTENTIAL). | 20 MW; 4C38138BFAED3FFO CRC64; |  |
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| 82       | 107                              | 110                              | 112                              | 204      | 308      | 363        | 399                      | 180                            | 44020                          |  |
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Query Match 66.7%; Score 389; DB 1; Length 399; Best Local Similarity 66.0%; Pred. No. 2.2e-32; Matches 70; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

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1.8 LGGPSVEIFPPRIKDVAMISLSPIVTCVVVDVSEDDPJOLISHS | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |

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